

SEQUENCE LISTING

<110> Diversa Corporation
Kerovuo, Janne
Solbak, Arne
Gray, Kevin
McCann, Ryan
Purohit, Shalaka
Gerendash, Joel
Janssen, Giselle
Dahod, Samun

<120> PECTATE LYASES, NUCLEIC ACIDS ENCODING
THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462009640

<140> To Be Assigned

<141> Concurrently herewith

<150> 60/460,842

<151> 2003-04-04

<150> 60/484,798

<151> 2003-07-03

<160> 134

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1917

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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180
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420
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480
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 840
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 960
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 1080
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 1320
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 1380
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 1440
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 1500
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 1620
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 1680
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 1740
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 1800
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<210> 2
 <211> 638
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(638)
 <223> Catalytic domain

<400> 2

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Ala	Asp	Gly	Ser	Gly	Asp	Val	Arg	Thr	Ile	Gln	Gln	Ala	Val	Asp	Gln
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Val	Pro	Lys	Asp	Asn	Thr	His	Pro	Val	Leu	Ile	Gln	Ile	Lys	Pro	Gly
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Val	Tyr	Gln	Glu	Gln	Val	Arg	Val	Ala	Ala	Gly	Lys	Arg	Phe	Ile	Thr
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Phe	Arg	Gly	Asp	Asp	Ala	Ser	Lys	Thr	Val	Ile	Thr	Tyr	Arg	Leu	Ser
				85					90					95	
Ala	Leu	Gln	Ala	Gly	Asn	Thr	Arg	Leu	Ala	Phe	Thr	Thr	Phe	Val	Asn
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Ala	Asp	Asp	Phe	Arg	Ala	Glu	Asn	Leu	Thr	Phe	Glu	Asn	Ser	Phe	Gly
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Thr	Gly	Ser	Gln	Ala	Val	Ala	Leu	Phe	Val	Asp	Ala	Asp	Arg	Ala	Thr
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Phe	Glu	Asn	Cys	Arg	Phe	Leu	Gly	Trp	Gln	Asp	Thr	Leu	Phe	Val	Asn
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Gly	Ser	Arg	His	Phe	Phe	Lys	Asp	Cys	Tyr	Val	Glu	Gly	His	Val	Asp
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Phe	Ile	Phe	Gly	Thr	Ala	Ser	Ala	Val	Phe	Glu	Asn	Cys	Thr	Ile	His
			180					185					190		
Ser	Lys	Gly	Glu	Gly	Tyr	Val	Thr	Ala	His	Tyr	Arg	Thr	Ser	Asp	Glu
		195					200					205			
Met	Asp	Thr	Gly	Phe	Val	Phe	His	Arg	Cys	Arg	Leu	Thr	Gly	Arg	Asp
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Thr	Gly	Arg	Gly	Val	Tyr	Leu	Gly	Arg	Pro	Trp	Arg	Pro	Tyr	Ala	Arg
225					230					235					240
Val	Val	Phe	Ile	Asp	Cys	Trp	Leu	Asp	Ala	His	Ile	Arg	Pro	Glu	Gly
				245					250					255	
Trp	Asp	Asn	Trp	Arg	Asp	Pro	Glu	Arg	Glu	Lys	Thr	Ala	Trp	Phe	Ala
			260					265					270		
Glu	Tyr	Lys	Ser	Lys	Gly	Pro	Gly	Ala	Asn	Pro	Val	Ala	Arg	Val	Ala
		275					280					285			
Trp	Ser	Arg	Gln	Leu	Thr	Thr	Glu	Gln	Ala	Ala	Glu	Phe	Ser	Arg	Glu
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Arg	Phe	Phe	Ser	Arg	Ala	Val	Arg	Gly	Leu	Ser	Gly	Gln	Ala	Asn	Gln
305					310					315					320
Ala	Val	Gly	Thr	Ile	Ala	Trp	Asp	Asp	Ala	Gln	Lys	Lys	Pro	Asn	Glu
				325					330					335	
Trp	Tyr	Ala	Ser	Ala	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Leu
			340					345					350		
Tyr	Gln	Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Gly	Lys
		355					360					365			
Pro	Leu	Asp	Glu	Lys	Gly	Arg	Ala	Gly	Leu	Leu	Arg	Val	Arg	Lys	Lys
	370					375					380				
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385					390					395					400
Leu	Ala	Arg	Val	Tyr	Thr	Ala	Gln	Lys	Gln	Glu	Arg	His	Arg	Glu	Ser
				405						410				415	
Phe	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Pro	Asn	Gly
			420					425					430		
Gly	Trp	Pro	Gln	Phe	Tyr	Pro	Asn	Leu	Asn	Gly	Tyr	Tyr	Lys	His	Ile
		435					440					445			

Thr	Phe	Asn	Asp	Asn	Ala	Met	Ile	Gly	Val	Met	Lys	Leu	Leu	Arg	Asp
450						455					460				
Val	Ala	Thr	Ala	Lys	Pro	Ala	Tyr	Ala	Phe	Val	Asp	Glu	Ala	Arg	Arg
465					470					475					480
Thr	Ser	Ala	Ala	Lys	Ala	Val	Glu	Lys	Gly	Ile	Glu	Cys	Ile	Leu	Lys
				485					490					495	
Thr	Gln	Val	Val	Val	Asn	Gly	Arg	Arg	Thr	Val	Trp	Cys	Ala	Gln	His
			500					505					510		
Asp	Glu	Val	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Thr	Phe	Glu	Leu	Val
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Ser	Leu	Ser	Gly	Gly	Glu	Ser	Val	Glu	Ile	Val	Arg	Phe	Leu	Met	Ser
	530					535					540				
Ile	Lys	Asn	Pro	Ser	Pro	Ala	Val	Val	Glu	Ala	Ile	Glu	Ser	Ala	Val
545					550					555					560
Ala	Trp	Phe	Glu	Gln	Ser	Gln	Val	Lys	Asp	Pro	Ala	Gly	Lys	Pro	Ala
				565					570					575	
Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Ala	Gly
			580					585					590		
Arg	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Lys	Gln	Ile	Asp	Glu	Glu	Arg
		595					600					605			
Arg	Lys	Asn	Tyr	Ala	Trp	Tyr	Val	Asp	Asp	Ala	Ala	Lys	Leu	Leu	Lys
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<210> 3

<211> 1416

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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atcgtgaaac gcatcaagcg acctcgtttc ccgatgcgca cgtttgatct cacggagttt
180
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240
tgcacgaacg ccggtggttg gagagtagtt gttccaccgg gttcgtatct cactggcgcc
300
attcatttga agagcaacgt cgaccttcat atctcagaag gtactacggt caagttcagc
360
cagaacccga aagactacct gcccgttggt ttctcgcgtt gggaaggcgt cgaggtgttc
420
aactactcgc cttttatcta cgccttcgaa caaacgaaca ttgcgatcac tggcaagggc
480
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540
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600
gaaaaaggtg tcccgttca ggagcgcatt tttggtgagg gccattactt aaggccgcag
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720
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840
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900
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960
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1080
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1200
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1260
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1320
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1416

<210> 4
<211> 471
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN
<222> (81)...(476)
<223> Catalytic domain

<400> 4
Met Ser Ser Arg Arg Glu Phe Ile Arg Asp Leu Leu Thr Gly Gly Ala
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Leu Ile Ala Val Ala Pro Arg Leu Ser Ala Phe Ala Ala Glu Glu Asn
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Pro Trp Glu Thr Val Met Pro Ser Ile Val Lys Arg Ile Lys Arg Pro
35 40 45
Arg Phe Pro Met Arg Thr Phe Asp Leu Thr Glu Phe Gly Ala Lys Gly
50 55 60
Asp Gly Arg Thr Asp Cys Thr Leu Ala Phe Arg Arg Ala Ile Asp Arg
65 70 75 80
Cys Thr Asn Ala Gly Gly Gly Arg Val Val Val Pro Pro Gly Ser Tyr
85 90 95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asp Leu His Ile Ser
100 105 110
Glu Gly Thr Thr Val Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
115 120 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
130 135 140
Phe Ile Tyr Ala Phe Glu Gln Thr Asn Ile Ala Ile Thr Gly Lys Gly
145 150 155 160
Thr Leu Asn Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
165 170 175
Arg Ala Ala Tyr Gly Trp Lys Glu Gly Met Ser Asn Gln Arg Pro Asp

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 660
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 720
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 780
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 900
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 960
 gtatccgaac cgaatgagtt gttgaatgaa gattatccga agtggaggac aaggagtgcg
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<210> 6
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(358)
 <223> Catalytic domain

<400> 6
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 Ser Trp Asn Glu Ile Leu Lys Gln Pro Lys Leu Trp Tyr Ala Val Asp
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 Glu Ala Thr Arg Ile Ala Asn Gln Val Ile Leu Tyr Gln Arg Asp Asn
 35 40 45
 Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Ala Met Leu Met Gln Ala
 50 55 60
 Glu Arg Glu Lys Leu Ser Arg Glu Lys Ser Glu Thr Asp Thr Thr Ile
 65 70 75 80
 Asp Asn Gly Ala Thr Thr Gln Leu Ala Tyr Leu Ala Lys Val Ile
 85 90 95
 Thr Ala Lys Asn Ile Glu Ser His Arg Val Ala Phe Phe Lys Gly Leu
 100 105 110
 Asp Phe Leu Phe Ala Met Gln Tyr Gly Asn Gly Gly Phe Pro Gln Phe
 115 120 125
 Phe Pro Leu Arg Asp Asp Tyr Ser Arg Glu Ile Thr Phe Asn Asp Asn
 130 135 140
 Ala Met Ile Asn Val Leu Arg Leu Leu Arg Asp Ile Ala Asp Arg Lys
 145 150 155 160
 Asn Asp Tyr Val Phe Val Asp Glu Glu Arg Arg Ala Lys Ala Glu Gln
 165 170 175
 Ala Val Arg Arg Ala Ile Pro Leu Ile Leu Ser Thr Gln Val Val Val
 180 185 190
 Asp Gly Lys Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Lys Thr Leu

	195						200					205							
Lys	Pro	Ala	Ala	Ala	Arg	Lys	Phe	Glu	Pro	Ala	Ser	Leu	Thr	Ala	Gly				
	210						215					220							
Glu	Ser	Val	Gly	Ile	Val	Arg	Phe	Leu	Met	Leu	Glu	Lys	Pro	Thr	Pro				
225						230					235				240				
Glu	Ile	Ile	Asn	Ala	Ile	Glu	Ser	Ala	Ile	Ala	Trp	Tyr	Lys	Ala	Asn				
			245						250					255					
Asn	Ile	Ser	Gly	Leu	Arg	Trp	Glu	Arg	Arg	Asn	Gly	Glu	Asn	Ile	Val				
			260					265					270						
Ile	Lys	Asp	Lys	Asn	Ala	Pro	Pro	Val	Trp	Ala	Arg	Phe	Tyr	Gln	Ile				
		275					280					285							
Glu	Thr	Met	Arg	Pro	Ile	Phe	Ala	Gly	Arg	Asp	Ala	Val	Ile	Arg	Tyr				
290						295					300								
Asp	Val	Met	Gln	Ile	Glu	Ser	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Tyr				
305					310					315					320				
Val	Ser	Glu	Pro	Asn	Glu	Leu	Leu	Asn	Glu	Asp	Tyr	Pro	Lys	Trp	Arg				
				325					330					335					
Thr	Arg	Ser	Ala	Lys	Arg	Ala	Gln	Ile	Phe	Gln	Arg	Pro	Pro	Leu	Gly				
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Ser	Arg	Phe	Arg	Thr	Val														
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<210> 7
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 120
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 180
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 240
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 780
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<210> 8
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(374)
 <223> Catalytic domain

<400> 8
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 Gln Ser Ala Ala Val Ser Gly Val Pro Ala Ala Ile Arg Trp Gly Ala
 35 40 45
 Asp Val Leu Arg Gln Lys Pro Glu Trp Tyr Ala Ser Arg Glu Ala Arg
 50 55 60
 Thr Ile Ala Asp Ser Val Ile Gln Tyr Gln Ala Ala Asp Gly Gly Trp
 65 70 75 80
 Pro Lys Asn Thr Asp Leu Gly Thr Pro Pro Thr Ala Glu Ser Arg Ala
 85 90 95
 Gly Ala Ala Ala Asp Val Thr Ser Ser Thr Ile Asp Asn Asn Gly Thr
 100 105 110
 Thr Met Pro Met Gln Phe Leu Ala Leu Val Ala Asp Ala Thr Gly Glu
 115 120 125
 Ala Arg Tyr Arg Ala Ser Phe Leu Arg Gly Phe Asp Tyr Leu Leu Ala
 130 135 140
 Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Phe Phe Pro Leu Arg Arg
 145 150 155 160
 Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asn Ala Met Val Asn Val
 165 170 175
 Leu Thr Val Leu Arg Asp Ala Ala Ala Gly Gln Ala Pro Tyr Ala Phe
 180 185 190
 Val Asp Glu Pro Arg Arg Ala Lys Ala Arg Ala Ala Val Ser Arg Gly
 195 200 205
 Ile Asp Val Ile Leu Lys Thr Gln Val Lys Gln Asn Gly Lys Leu Thr
 210 215 220
 Ala Trp Cys Ala Gln His Asp Glu Lys Thr Leu Ala Pro Ala Trp Ala
 225 230 235 240
 Arg Ala Tyr Glu Pro Pro Ser Leu Ser Gly Ser Glu Thr Val Gly Ile
 245 250 255
 Val Arg Phe Leu Met Glu Ile Glu Lys Pro Ser Pro Glu Ile Val Ala
 260 265 270
 Ala Ile Glu Gly Ala Val Ala Trp Leu Lys Ser Val Ala Ile Pro Gly
 275 280 285
 Leu Arg Tyr Glu Ser Phe Thr Gly Ala Asp Gly Gln Arg Asp Arg Arg
 290 295 300
 Val Val Pro Asp Pro Ser Ala Gly Leu Leu Trp Ala Arg Phe Tyr Glu

305					310					315				320
Leu	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Leu	Gly	Arg	Asp	Ser	Val	Val Arg
				325					330					335
Ala	Ala	Leu	Ser	Asp	Ile	Glu	Arg	Glu	Arg	Arg	Ala	Gly	Tyr	Ala Tyr
			340					345					350	
Tyr	Gly	Thr	Trp	Pro	Ala	Ser	Leu	Ile	Ala	Ala	Asp	Tyr	Pro	Arg Trp
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Arg	Ser	Thr	Leu	Arg	Arg									
	370													

<210> 9
 <211> 1116
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 120
 ctaaaccaaa aacctgcctg gtacggcagc ccggaagcgg tgcgcattgc tgacaacctg
 180
 ttgctttacc aacgcgacca cggcggctgg cacaagaata tcgaaatggc tgcggtcttg
 240
 accgaacagc aacaggcaga gttgaaagcg caaaaggcaa ccgacgattc gacgattgat
 300
 aacggcgcgga cctataccca ggtgatttat ctggcgcgcg tcttcaatgc gacgaagcag
 360
 gagcgattca aaaccgcgtt tctcaaagga ttcgattatc tgctcaaggc tcagtatgcy
 420
 aacggcgggt ggccgcagta ttaccgcgtt ttgcagggtt attacaaaca catcacgttc
 480
 aacgatgacg cgatggtcgg cgtgcttgat cttctgcgcg atgttgcgcg cggcgattcc
 540
 gggttatcgg tctggtgacg cgaccggcgc gcccgcgcca gccaggccgt gcaaaaagga
 600
 attgagtga tcttgaaatg ccagatcgtg gtcgccggga aaaagaccgc ctggtgcgcg
 660
 caacacgatg aagtgcatt cgccccgcg ccggcacgca cctacgagaa aatttcgctg
 720
 agcggcagcg aatcggttg cctgatccgc ttcctgatgg gcattgaaca accggacgcy
 780
 cgtgtagttg aggcgattga gtccgccgtt gcctggctca agcaagccaa gctgaccggc
 840
 atcaaagtgg ttcagaaggc ggatgcttcg aagcccaatg gcttcgaccg ggtcgctcgtt
 900
 gaagatgcac aagccggggc attgtgggcy cgctttttacg agatcggtac gggccgcccc
 960
 atcttttccg gacgtgacgg catcgtcaaa tacagcttg cggaaatcga acacgaacgy
 1020
 cgcacgggct acggctggta cacgaatgcg cccgcgaaat tgctggaaca agattatccg
 1080
 gcctggcaaa tcaaacgcgy gggcaagaaa aagtaa
 1116

<210> 10
 <211> 371
 <212> PRT

<220>

<221> SIGNAL

<221> DOMAIN

<223> Catalytic domain

[illegible]

<210> 11
<211> 1167
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 11
atgtcgttgg gaccaggtgc taatccgaaa gtcgcggttc cctgggtccaa acaactatcg
60
ggtggttgagg caaagttggt cgatcgcgag cggttcttca gcctcgtgc ggaacgaacc
120
tctaagaaga atgaccagca agtcggcgcc atcgcgtgga aagatgcaca cggaaaggca
180
gatgagtggg atgcgagcgt tgaggcactt cgtatagccg ataacgtcgt tttctatcaa
240
cgtgactcag gtggctggcc caagaatatc gagatggcga agacgttgag cgatcgtgag
300
aaggctgcga ttctccgcga gaagaaaaag aatgactcaa caatcgacaa tggcgcgact
360
cacactcagt tatcttttct ggcgcgctc tatacagcac aacagcagga gcgacatcgc
420
gagtcatttt taaaaggact ggattactta ctgaaggcgc agtattcaaa tgggtggctgg
480
ccacagttct atccaaactt gaatggctac taaaaacgga tcacgtacaa cgatggcgcg
540
atgatcggtg tgatgaagct tctgcgtgat gttgcggcag cgaaacctga atacgcgttt
600
gtcgtatgaaa ctccggcgtgc gaaggctgcg aacgcggtgg aaaaaggcat cgtgtgcatt
660
ttgaaaacgc aggtggttgt tgatgggcgt cgcactgttt ggtgtgcaca acacgacgaa
720
gtgacgtttg cgcccgcgcc tgcaagaaag tttgagttag cttcgttgag cggcggtgag
780
agcgtcgata ttgttcgatt tctaattgtcg ataaaggatc catcgcgtaa cgtggttgaa
840
tcgattgaat cggcagttaa atggtttgag cagtcggagc taaaaggcgt taagtgggtc
900
aagaaaaccg acgctactca acctaattggg ttcgattgtg tcgttggttaa agatccggag
960
agctctgttt gggcgcgctt ttacgagatt ggcacgaacc gcccgatctt tgccggggcgt
1020
gatggagtgc ctaagtatga cgtcgcgcag atcgaacacg agcgacgaac gggttacgaa
1080
tggtacgttg atgaggcagc aaaactgctg aaaaaagatt atccggcgtg gaagaaacga
1140
catgtcgtca cgacgcgagt tcattag
1167

<210> 12
<211> 388
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(388)

<223> Catalytic domain

<400> 12

Met Ser Leu Gly Pro Gly Ala Asn Pro Lys Ala Arg Val Pro Trp Ser
1 5 10 15
Lys Gln Leu Ser Gly Val Glu Ala Lys Leu Phe Asp Arg Glu Arg Phe
20 25 30
Phe Ser Leu Ala Ala Glu Arg Thr Ser Lys Lys Asn Asp Gln Gln Val
35 40 45
Gly Ala Ile Ala Trp Lys Asp Ala His Gly Lys Ala Asp Glu Trp Tyr
50 55 60
Ala Ser Val Glu Ala Leu Arg Ile Ala Asp Asn Val Val Phe Tyr Gln
65 70 75 80
Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Glu Met Ala Lys Thr Leu
85 90 95
Ser Asp Arg Glu Lys Ala Ala Ile Leu Arg Glu Lys Lys Lys Asn Asp
100 105 110
Ser Thr Ile Asp Asn Gly Ala Thr His Thr Gln Leu Ser Phe Leu Ala
115 120 125
Arg Val Tyr Thr Ala Gln Gln Gln Glu Arg His Arg Glu Ser Phe Leu
130 135 140
Lys Gly Leu Asp Tyr Leu Leu Lys Ala Gln Tyr Ser Asn Gly Gly Trp
145 150 155 160
Pro Gln Phe Tyr Pro Asn Leu Asn Gly Tyr Tyr Lys Arg Ile Thr Tyr
165 170 175
Asn Asp Gly Ala Met Ile Gly Val Met Lys Leu Leu Arg Asp Val Ala
180 185 190
Ala Ala Lys Pro Glu Tyr Ala Phe Val Asp Glu Thr Arg Arg Ala Lys
195 200 205
Ala Ala Asn Ala Val Glu Lys Gly Ile Val Cys Ile Leu Lys Thr Gln
210 215 220
Val Val Val Asp Gly Arg Arg Thr Val Trp Cys Ala Gln His Asp Glu
225 230 235 240
Val Thr Phe Ala Pro Ala Pro Ala Arg Lys Phe Glu Leu Ala Ser Leu
245 250 255
Ser Gly Gly Glu Ser Val Asp Ile Val Arg Phe Leu Met Ser Ile Lys
260 265 270
Asp Pro Ser Arg Asn Val Val Glu Ser Ile Glu Ser Ala Val Lys Trp
275 280 285
Phe Glu Gln Ser Glu Leu Lys Gly Val Lys Trp Val Lys Lys Thr Asp
290 295 300
Ala Thr Gln Pro Asn Gly Phe Asp Cys Val Val Val Lys Asp Pro Glu
305 310 315 320
Ser Ser Val Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile
325 330 335
Phe Ala Gly Arg Asp Gly Val Pro Lys Tyr Asp Val Ala Gln Ile Glu
340 345 350
His Glu Arg Arg Thr Gly Tyr Glu Trp Tyr Val Asp Glu Ala Ala Lys
355 360 365
Leu Leu Lys Lys Asp Tyr Pro Ala Trp Lys Lys Arg His Val Val Thr
370 375 380
Thr Arg Val His
385

<210> 13

<211> 1065

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 13
atgaaaacga tcagccttat ttgcctcgca atctctgctg ggattctgga ttcggttgcg
60
gcggcacgct ggaacgaatt cgcccagaag gcggatgatt ggtatcgagg tgacgaaggc
120
aggcgcggtg cttcgaatat tctttctcac caatcactgc aaggaagctg gcccagaagt
180
accgatacca ccgcgagatt cttcaatgga gatctagcga agattcaggg cacgttcgac
240
aacggtgcga cgacggacga gttgcgtttc ctggcccgcg cgtttgtcgc cacgaaagaa
300
aaaaactacg agtcagcggt ccgaaaaggc ttcgaacaca ttctcgcggc gcaatacgcg
360
aacggcggat ggccgcaata ttcgccgccg cccaaaagtt accaccgaca cattaccttc
420
aacgataatt cgatggtgcg gctgatgatt ttccttcgcg aggtcacgac ttcgaatctc
480
tactcgttcg tcgaagcgcc gctgcgaaca caagcccgcg aaagtttcga tcgcggtgtg
540
cgggtgcattc ttaagtgccg gatcgctcgtg aacgggcaca agaccgcgtg gtgcgcgcaa
600
catgatgaaa cggatttcag ccccgatcc gcgcgtagtt acgaactgcc ttcgctgagc
660
ggttctgaat cagtcggcat tgtgcgcttg ctgatgagcc tcgatcagcc gagccgcgga
720
gtgatcgatg ccatcaccaa cgccgtagcg tggttcgaat cggcgaagct gcccgggatc
780
aaaaccgttc aagagaccga tccgaattcg cccaaaggct ggaatcgctg cgtcgtaaaa
840
gatgaaagtg cccgaccgat gtgggcgcgt ttctacgaca tcaacaccaa caaaccgttc
900
ttttgtgatc gcgatggtgt gccaaagccg agtcttgccg agatcggtta tgaacggcgg
960
aacggttatg cgtggctcgg atactggcct gaagacttgc tcgcaagaga gtatccagcg
1020
tggaagatga agtggctgaa gcccaaagag cgcccagcat tttga
1065

<210> 14
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(354)
<223> Catalytic domain

<400> 14
Met Lys Thr Ile Ser Leu Ile Cys Leu Ala Ile Ser Ala Gly Ile Leu
1 5 10 15
Asp Ser Val Ala Ala Arg Trp Asn Glu Phe Ala Gln Lys Ala Asp
20 25 30
Asp Trp Tyr Arg Gly Asp Glu Gly Arg Arg Val Ala Ser Asn Ile Leu
35 40 45

Ser	His	Gln	Ser	Leu	Gln	Gly	Ser	Trp	Pro	Lys	Asn	Thr	Asp	Thr	Thr
50						55					60				
Ala	Arg	Phe	Phe	Asn	Gly	Asp	Leu	Ala	Lys	Ile	Gln	Gly	Thr	Phe	Asp
65					70					75					80
Asn	Gly	Ala	Thr	Thr	Asp	Glu	Leu	Arg	Phe	Leu	Ala	Arg	Ala	Phe	Val
				85					90					95	
Ala	Thr	Lys	Glu	Lys	Asn	Tyr	Glu	Ser	Ala	Phe	Arg	Lys	Gly	Phe	Glu
			100					105					110		
His	Ile	Leu	Ala	Ala	Gln	Tyr	Ala	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Ser
		115					120					125			
Pro	Pro	Pro	Lys	Ser	Tyr	His	Arg	His	Ile	Thr	Phe	Asn	Asp	Asn	Ser
	130					135					140				
Met	Val	Arg	Leu	Met	Ile	Phe	Leu	Arg	Glu	Val	Thr	Thr	Ser	Asn	Leu
145					150					155					160
Tyr	Ser	Phe	Val	Glu	Ala	Pro	Leu	Arg	Thr	Gln	Ala	Arg	Glu	Ser	Phe
				165					170					175	
Asp	Arg	Gly	Val	Arg	Cys	Ile	Leu	Lys	Cys	Gln	Ile	Val	Val	Asn	Gly
			180					185					190		
His	Lys	Thr	Ala	Trp	Cys	Ala	Gln	His	Asp	Glu	Thr	Asp	Phe	Ser	Pro
		195					200					205			
Arg	Ser	Ala	Arg	Ser	Tyr	Glu	Leu	Pro	Ser	Leu	Ser	Gly	Ser	Glu	Ser
	210					215					220				
Val	Gly	Ile	Val	Arg	Leu	Leu	Met	Ser	Leu	Asp	Gln	Pro	Ser	Arg	Gly
225					230					235					240
Val	Ile	Asp	Ala	Ile	Thr	Asn	Ala	Val	Ala	Trp	Phe	Glu	Ser	Ala	Lys
				245					250					255	
Leu	Pro	Gly	Ile	Lys	Thr	Val	Gln	Glu	Thr	Asp	Pro	Asn	Ser	Pro	Lys
			260					265					270		
Gly	Trp	Asn	Arg	Val	Val	Val	Lys	Asp	Glu	Ser	Ala	Arg	Pro	Met	Trp
		275					280					285			
Ala	Arg	Phe	Tyr	Asp	Ile	Asn	Thr	Asn	Lys	Pro	Phe	Phe	Cys	Asp	Arg
	290					295					300				
Asp	Gly	Val	Pro	Lys	Pro	Ser	Leu	Ala	Glu	Ile	Gly	Tyr	Glu	Arg	Arg
305					310					315					320
Asn	Gly	Tyr	Ala	Trp	Leu	Gly	Tyr	Trp	Pro	Glu	Asp	Leu	Leu	Ala	Arg
				325					330					335	
Glu	Tyr	Pro	Ala	Trp	Lys	Met	Lys	Trp	Leu	Lys	Pro	Lys	Glu	Arg	Pro
			340					345					350		
Ala	Phe														

<210> 15
 <211> 1575
 <212> DNA
 <213> Bacteria

<400> 15
 atgagacgac cagtcgcact ccggtccac gcggcactgg ccaccctggc cctggcggcc
 60
 gcgaccggcg tgggtctctc gatccccag gcatcggcgg cggccggcgg cgccaccggc
 120
 tacgccggcc agaacggcgg caccaccggc ggtgccggcg gccagaccgt acgggccacc
 180
 acgggcaccg ccatccacgc ggccctgtgc ggacgggcca gcagcagcac cccgatcacg
 240
 atcgaggtcg agggaacgat caaccacgcc aacaccgcca aggtgtccgg cccagctgc
 300
 aacaccgccc ccggagtgat cgagctgaag cagatcagca acgtcacgct cgtcggggtc
 360
 ggctccggcg ccgtcttcga ccaactcggc atccacatcc gcgagtccag caacatcatc
 420

atccagaacg tgacggtccg gaacgtcaag aagtcgggct cgccgctgtc caacggcggc
 480
 gacgccatcg gcatggagag cgacgtccgc aacgtctggg tcgaccactc caccctggag
 540
 gcctcgggcg gcgagtccga gggctacgac ggcctcttcg acatgaagga caacacccgg
 600
 tacgtgacct tgtcgtacag catcctgcgc aaatccgggc gcggcggcct cgtgggggtcc
 660
 agcgagaccg aactctcgaa cagcttcacg acgtaccacc acaacctgta cgagaacatc
 720
 gactcgcgcg cgcccctgct gcgcggcggg accgcccaca tgtacaacaa ccactacctg
 780
 cggatcaacg agtccggcat caactcccggt gccggagccc acgccaaggt ggacaacaac
 840
 tacttcgagg actccaagga cgtcctcggc accttctaca ccgacgccgc cgggtactgg
 900
 caggtcagcg gcaacgtcta cgacaacgtg acctggtccg cccggggcac cgacaacaac
 960
 ccggcggggc cggaccgcga gtccaacacc accgtctcca tcccctacgc cttcagcctc
 1020
 gacccggcca cctgcgtgcc ggacgtcgtg agccgaacgg cgggtgccgg caagggactt
 1080
 caggtgtcga acggcagctg ctccccgcag acaccacgc ccacgccgac gggcacgccg
 1140
 accacacccg cgccgacgac tcccaccccg agcccgacgc cctccacgcc cggaccgacc
 1200
 cagcccggcg ggacgaacct cagcatcggt gccgggtccg acggttcgag caagggccgac
 1260
 ggcaccagct acggcaacgt ccgggacggg gacctcggca cccactggtc tccggccggg
 1320
 tcgaccggct ccgtgtcgat caagtggggc agcgccacca cggctctccc catcgtcatc
 1380
 cgcgaggcgg cgggcgcgac gggcgtcatc ggctcctggc tcgtcctgaa cggcgacacc
 1440
 ggcgccgtgc tgacctccg cagcggggcg gggacgatct ccgtcccccg gacggccctg
 1500
 aagaagatca ccttcgagat cacgggcgcg agcggcacgc cacggatcgc cgagttcgag
 1560
 acgtacgccg gctag
 1575

<210> 16
 <211> 524
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(33)

<221> DOMAIN
 <222> (34)...(359)
 <223> Catalytic domain

<400> 16
 Met Arg Arg Pro Val Ala Leu Arg Leu His Ala Ala Leu Ala Thr Leu
 1 5 10 15
 Ala Leu Ala Ala Ala Thr Gly Val Val Leu Ser Ile Pro Gln Ala Ser
 20 25 30
 Ala Ala Ala Gly Gly Ala Thr Gly Tyr Ala Gly Gln Asn Gly Gly Thr

		35					40					45				
Thr	Gly	Gly	Ala	Gly	Gly	Gln	Thr	Val	Arg	Ala	Thr	Thr	Gly	Thr	Ala	
Ile	His	Ala	Ala	Leu	Cys	Gly	Arg	Ala	Ser	Ser	Ser	Thr	Pro	Ile	Thr	
65					70					75					80	
Ile	Glu	Val	Glu	Gly	Thr	Ile	Asn	His	Ala	Asn	Thr	Ala	Lys	Val	Ser	
				85					90					95		
Gly	Pro	Ser	Cys	Asn	Thr	Ala	Ala	Gly	Val	Ile	Glu	Leu	Lys	Gln	Ile	
			100					105					110			
Ser	Asn	Val	Thr	Leu	Val	Gly	Val	Gly	Ser	Gly	Ala	Val	Phe	Asp	Gln	
		115				120						125				
Leu	Gly	Ile	His	Ile	Arg	Glu	Ser	Ser	Asn	Ile	Ile	Ile	Gln	Asn	Val	
	130					135					140					
Thr	Val	Arg	Asn	Val	Lys	Lys	Ser	Gly	Ser	Pro	Leu	Ser	Asn	Gly	Gly	
145					150					155					160	
Asp	Ala	Ile	Gly	Met	Glu	Ser	Asp	Val	Arg	Asn	Val	Trp	Val	Asp	His	
				165					170					175		
Ser	Thr	Leu	Glu	Ala	Ser	Gly	Gly	Glu	Ser	Glu	Gly	Tyr	Asp	Gly	Leu	
			180					185					190			
Phe	Asp	Met	Lys	Asp	Asn	Thr	Arg	Tyr	Val	Thr	Leu	Ser	Tyr	Ser	Ile	
		195					200					205				
Leu	Arg	Lys	Ser	Gly	Arg	Gly	Gly	Leu	Val	Gly	Ser	Ser	Glu	Thr	Glu	
	210					215					220					
Leu	Ser	Asn	Ser	Phe	Ile	Thr	Tyr	His	His	Asn	Leu	Tyr	Glu	Asn	Ile	
225					230					235					240	
Asp	Ser	Arg	Ala	Pro	Leu	Leu	Arg	Gly	Gly	Thr	Ala	His	Met	Tyr	Asn	
				245					250					255		
Asn	His	Tyr	Leu	Arg	Ile	Asn	Glu	Ser	Gly	Ile	Asn	Ser	Arg	Ala	Gly	
			260					265					270			
Ala	His	Ala	Lys	Val	Asp	Asn	Asn	Tyr	Phe	Glu	Asp	Ser	Lys	Asp	Val	
		275					280					285				
Leu	Gly	Thr	Phe	Tyr	Thr	Asp	Ala	Ala	Gly	Tyr	Trp	Gln	Val	Ser	Gly	
	290					295					300					
Asn	Val	Tyr	Asp	Asn	Val	Thr	Trp	Ser	Ala	Arg	Gly	Thr	Asp	Asn	Asn	
305					310					315					320	
Pro	Ala	Gly	Pro	Asp	Pro	Gln	Ser	Asn	Thr	Thr	Val	Ser	Ile	Pro	Tyr	
				325					330					335		
Ala	Phe	Ser	Leu	Asp	Pro	Ala	Thr	Cys	Val	Pro	Asp	Val	Val	Ser	Arg	
			340					345					350			
Thr	Ala	Gly	Ala	Gly	Lys	Gly	Leu	Gln	Val	Ser	Asn	Gly	Ser	Cys	Ser	
		355					360					365				
Pro	Gln	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Pro	Thr	Thr	Pro	Ala	
	370					375					380					
Pro	Thr	Thr	Pro	Thr	Pro	Ser	Pro	Thr	Pro	Ser	Thr	Pro	Gly	Pro	Thr	
385					390					395					400	
Gln	Pro	Gly	Gly	Thr	Asn	Leu	Ser	Ile	Gly	Ala</						

<210> 17
<211> 1047
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 17
ttgccgcgtg cgcccgggtg tgagtcgtca tcgccagcgc agacgtcatc ggttgcggtc
60
tcctgggatc agatcctccg tcagcctgcg gcctggtacg gcggtgcgga ggcgttgcca
120
gtcgctgaga acgtgctctt gtatcagcgc gcggcaggag ggtggccgaa gaacatcaac
180
atggcgggcg cgatgaccgc cgctgaccgt gcgaaagtca cggacgagcg cgcgcagaac
240
gacgccacga tcgacaacac gtcaacgacg acgcagatcc gttttcttgc gctcgttctt
300
cgcggcaccg ccgacgcacg attcaaggac gcggcgctga agggcatcga cttcctgctg
360
gctgcgcaat acgcgaatgg aggctggcct cagtattttc ccctgcgcga cgactactcg
420
cggcgcatca cgttcaatga cgacgcgatg gtgaatgtga tgacgctgct gcgcgagact
480
tcgcagggcc agacgccgtt cgagttcgtc gacgcctcgc ggcgcgggccg ggcggcgcag
540
tctgtctcac gcggcgctga cgtcatgctg cgcacgcaga ttcgagtcaa cggcgtgctg
600
accggctggt gccagcagca cgacgagcgg aactttcagc cgggtgaaggc gcgcgcgtac
660
gaacatccgt cgattgccag caaggaaacc gcgagcatcg caagattcct gatggggatt
720
gaacggccgt cgccggagat cgtgtccgcg gtggatggcg cagtcgctg gttgcgagcg
780
gcgcagattt cagggtgtcg gacggagcgc cggcccgcgc gatcgaatcc gggcggcgac
840
gtcgtggcgg tgcaggactc cgccgcgccg ccaatctggg cccgcttcta cgagattggc
900
accaaccggc cgatgttttc gggtcgcgac ggcgtcatca agtacagcct cagcgagatc
960
gagatcgagc ggcgcgctgg atacagctgg tacggcgact acgccgccag actgctcaga
1020
gacgactatc cgaagtggaa gaaatga
1047

<210> 18
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(348)
<223> Catalytic domain

<400> 18
Met Pro Arg Ala Pro Gly Gly Glu Ser Ser Ser Pro Ala Gln Thr Ser

1	5	10	15
Ser Val Ala Val Ser Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp			
	20	25	30
Tyr Gly Gly Ala Glu Ala Leu Arg Val Ala Glu Asn Val Leu Leu Tyr			
	35	40	45
Gln Arg Ala Ala Gly Gly Trp Pro Lys Asn Ile Asn Met Ala Ala Pro			
	50	55	60
Met Thr Ala Ala Asp Arg Ala Lys Val Thr Asp Glu Arg Ala Gln Asn			
65	70	75	80
Asp Ala Thr Ile Asp Asn Thr Ser Thr Thr Thr Gln Ile Arg Phe Leu			
	85	90	95
Ala Leu Val Leu Arg Gly Thr Ala Asp Ala Arg Phe Lys Asp Ala Ala			
	100	105	110
Leu Lys Gly Ile Asp Phe Leu Leu Ala Ala Gln Tyr Ala Asn Gly Gly			
	115	120	125
Trp Pro Gln Tyr Phe Pro Leu Arg Asp Asp Tyr Ser Arg Arg Ile Thr			
	130	135	140
Phe Asn Asp Asp Ala Met Val Asn Val Met Thr Leu Leu Arg Glu Thr			
145	150	155	160
Ser Gln Gly Gln Thr Pro Phe Glu Phe Val Asp Ala Ser Arg Arg Gly			
	165	170	175
Arg Ala Ala Gln Ser Val Ser Arg Gly Val Asp Val Met Leu Arg Thr			
	180	185	190
Gln Ile Arg Val Asn Gly Val Leu Thr Gly Trp Cys Gln Gln His Asp			
	195	200	205
Glu Arg Asn Phe Gln Pro Val Lys Ala Arg Ala Tyr Glu His Pro Ser			
	210	215	220
Ile Ala Ser Lys Glu Thr Ala Ser Ile Ala Arg Phe Leu Met Gly Ile			
225	230	235	240
Glu Arg Pro Ser Pro Glu Ile Val Ser Ala Val Asp Gly Ala Val Ala			
	245	250	255
Trp Leu Arg Ala Ala Gln Ile Ser Gly Val Arg Thr Glu Arg Arg Pro			
	260	265	270
Asp Gly Ser Asn Pro Gly Gly Asp Val Val Ala Val Gln Asp Ser Ala			
	275	280	285
Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro			
	290	295	300
Met Phe Ser Gly Arg Asp Gly Val Ile Lys Tyr Ser Leu Ser Glu Ile			
305	310	315	320
Glu Ile Glu Arg Arg Ala Gly Tyr Ser Trp Tyr Gly Asp Tyr Ala Ala			
	325	330	335
Arg Leu Leu Arg Asp Asp Tyr Pro Lys Trp Lys Lys			
	340	345	

<210> 19
 <211> 1122
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 19
 gtgaacaggt ggcgcgaaga cttcttgccg gacttcgcgg cccgcatgct ccggtgcatg
 60
 gttccccggc cgcagatcca ctggggcggc ggtgtcatcc ggcaggaacc ggaatggtac
 120
 ggctcggccg aggcgcgtgc gatcgccgac agcggttcttc aataccagtc gaccgctggc
 180
 ggctggccca agaacaccga cttgacggtc tcgccaccgt ccgccgaatt ccttgccgat
 240

gcggatggtc tcacgaacac gatcgacaac gacgccacca cgttgccgat gcgattttctc
 300
 gctctgggtg cgcacgcgac cggcggcatc aagtaccgcg ccgcgttcga acgcggtctg
 360
 gactacctgc tcgccgetca gtatcccaat ggcggctggc ctcagtattt tcccctgcgt
 420
 gacggctatt actcgcacat cacctacaac gacaatgcga tgggtcaacgt cctcaccgtt
 480
 ctgcgcgatg cggccgcggg ccggcccccct tactcgttcg tcgacagggc ccggcgcgccc
 540
 agagcagaaa cggccatcgc tcgcggcatc gacatcatcg tgcgcactca ggtgagacgg
 600
 gccggcgtgc tgaccgcgtg gtgcgcccag cacgacgaaa agacgctcga gccggcgtgg
 660
 gcgcgcaact acgaaccgcc gacactctcc gggcacgaaa gcgtcggcat cgtgcgcttt
 720
 ctcatgggaa tcgaaaagcc cacgccgagg atcgtcgcgg cgggtgcaagg cgccgctgac
 780
 tggttgagag ccgtcgcgat cagcgggttg cgtctcgagg aattcaccga cgccgatggc
 840
 aggcgcgaca ggcgcgctcg cgccgatccg gcagcgccgc tcctgtgggc gcgcttctac
 900
 gagcttgcca cggaccgtcc cgtcttcacc ggccgcgaca aggtgatccg gtactcgctc
 960
 agcgaatcgc agcacgagcg ccggaacggg tatgcctact atggcacatg gccggccacg
 1020
 ctctcagcg aggtatccc ccgttggcgc gcgaaacacc tggctcgacg gagcgtcagg
 1080
 caggtagagg agggaatcgc gatacgcgtc cctaattccct ga
 1122

<210> 20

<211> 373

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(373)

<223> Catalytic domain

<400> 20

Met	Asn	Arg	Trp	Arg	Glu	Asp	Phe	Leu	Arg	Asp	Phe	Ala	Ala	Arg	Met
1				5					10					15	
Leu	Arg	Cys	Met	Val	Pro	Arg	Pro	Gln	Ile	His	Trp	Gly	Gly	Gly	Val
		20						25					30		
Ile	Arg	Gln	Glu	Pro	Glu	Trp	Tyr	Gly	Ser	Ala	Glu	Ala	Arg	Ala	Ile
		35					40					45			
Ala	Asp	Ser	Val	Leu	Gln	Tyr	Gln	Ser	Thr	Ala	Gly	Gly	Trp	Pro	Lys
	50					55					60				
Asn	Thr	Asp	Leu	Thr	Val	Ser	Pro	Pro	Ser	Ala	Glu	Phe	Leu	Ala	Asp
65					70				75					80	
Ala	Asp	Gly	Leu	Thr	Asn	Thr	Ile	Asp	Asn	Asp	Ala	Thr	Thr	Leu	Pro
			85					90						95	
Met	Arg	Phe	Leu	Ala	Leu	Val	Ala	His	Ala	Thr	Gly	Gly	Ile	Lys	Tyr
		100						105					110		
Arg	Ala	Ala	Phe	Glu	Arg	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr
	115					120						125			
Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Phe	Pro	Leu	Arg	Asp	Gly	Tyr	Tyr

130		135		140
Ser His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Val				
145		150		155
Leu Arg Asp Ala Ala Gly Arg Pro Pro Tyr Ser Phe Val Asp Arg				160
	165		170	
Ala Arg Arg Ala Arg Ala Glu Thr Ala Ile Ala Arg Gly Ile Asp Ile				175
	180		185	
Ile Val Arg Thr Gln Val Arg Arg Ala Gly Val Leu Thr Ala Trp Cys				190
	195		200	
Ala Gln His Asp Glu Lys Thr Leu Glu Pro Ala Trp Ala Arg Asn Tyr				205
	210		215	
Glu Pro Pro Thr Leu Ser Gly His Glu Ser Val Gly Ile Val Arg Phe				220
225			230	
Leu Met Gly Ile Glu Lys Pro Thr Pro Arg Ile Val Ala Ala Val Gln				235
	245		250	
Gly Ala Ala Asp Trp Leu Arg Ala Val Ala Ile Ser Gly Leu Arg Leu				255
	260		265	
Glu Glu Phe Thr Asp Ala Asp Gly Arg Arg Asp Arg Arg Val Val Ala				270
	275		280	
Asp Pro Ala Ala Pro Leu Leu Trp Ala Arg Phe Tyr Glu Leu Gly Thr				285
	290		295	
Asp Arg Pro Val Phe Thr Gly Arg Asp Lys Val Ile Arg Tyr Ser Leu				300
305			310	
Ser Glu Ile Glu His Glu Arg Arg Asn Gly Tyr Ala Tyr Tyr Gly Thr				315
	325		330	
Trp Pro Ala Thr Leu Leu Ser Glu Glu Tyr Pro Arg Trp Arg Ala Lys				335
	340		345	
His Leu Ala Arg Arg Ser Val Arg Gln Val Glu Glu Gly Ile Ala Ile				350
	355		360	
Arg Val Pro Asn Pro				365
370				

<210> 21
 <211> 1269
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 21
 atgcgtaaat cgaactgggc cgtcacaacg gccatcctgc tcgcgctgag cgccgcaccg
 60
 ctggcggaag agcccatcgg acagatcacc ctgcgccgtgc cgctcagccc ggcgcgcctg
 120
 accgaaaacgc cgcctgagca gcgggacgaa tggcaggcct atctcgccac caccgaggca
 180
 cagcttaagg cagacaaggc ggcgctggct gccgagcgcg ccggtctggc cgaaatcccc
 240
 gccaaagccga agaccggcag cgccaacacc atgccgctcg acaagccgct ggaatggtac
 300
 gcgtcgtccg aggcgcgtct ggtcgcgat aatatcgtca gctatcagac tccggcaggc
 360
 ggctggggca aaaatcaggc ccgcaacgaa cccacgcggt tgaaaggatca ggcctacact
 420
 atcgatgacg ccgatccac cggttcgggc aaatggaact tcgtcggcac catcgacaac
 480
 gacgccacca tcgtggaaat tcgctttctc gcccgcgtag cggcggcggc cacgggcccc
 540
 gaaggcgacg tctatcgcg ctcgccacg cgcgccatca cctacttgct ggcggcgacg
 600

taccccaatg gcggctggcc gcaggtctgg ccgcttcagg gcggctatca cgacgccatc
 660
 accctcaatg acggcgcgat gatccatgtg ctcgaactgt ttgacgacat cgccagcgga
 720
 cagggcgact tcgccttcct gcctgagccg ctgcgcgaca aggtcgaggc cgcacaggca
 780
 aagggtcaga aggtgcttct cgatcttcag cttaagcgca acggcgaacg caccctgtgg
 840
 gcgcagcagt acgatccgat taccctcttg cccagcgcgg cgcgtaacta cgagccgtcg
 900
 tcgatcagca ccggtgaaag cgccggtgtg ctgatctacc tcatgtccct gcccaacccc
 960
 tcgcctgaag tgcgcgacgc catcgaaaaa ggcgtggccc tgctgatcaa acttcagatc
 1020
 aacggcatgg catgggaaaa ggacggcatg cgaaacgtc tggtcgcaa ggctgacgcc
 1080
 tcgccgctgt ggtcgcgcta tcacgactcg gaaacgctgc tgcccattct cggtgaccgc
 1140
 gacatgcgca tcttcgacga cgtcaacgac atcagcgacg aacgcagccg cggctatgcc
 1200
 tggatatggca caagcccggc acggggccatc gccgaatacg aaaaatggaa acagggcaac
 1260
 ggcaaatga
 1269

<210> 22
 <211> 422
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(23)

<221> DOMAIN
 <222> (24)...(422)
 <223> Catalytic domain

<400> 22
 Met Arg Lys Ser Asn Trp Ala Val Thr Thr Ala Ile Leu Leu Ala Leu
 1 5 10 15
 Ser Ala Ala Pro Leu Ala Ala Lys Pro Ile Gly Gln Ile Thr Leu Ala
 20 25 30
 Val Pro Leu Ser Pro Ala Arg Leu Thr Glu Thr Pro Pro Glu Gln Arg
 35 40 45
 Ala Gln Trp Gln Ala Tyr Leu Ala Thr Thr Glu Ala Gln Leu Lys Ala
 50 55 60
 Asp Lys Ala Ala Leu Ala Ala Glu Arg Ala Gly Leu Ala Glu Ile Pro
 65 70 75 80
 Ala Lys Pro Lys Thr Gly Ser Ala Asn Thr Met Pro Leu Asp Lys Pro
 85 90 95
 Leu Glu Trp Tyr Ala Ser Ser Glu Ala Arg Leu Val Ala Asp Asn Ile
 100 105 110
 Val Ser Tyr Gln Thr Pro Ala Gly Gly Trp Gly Lys Asn Gln Ala Arg
 115 120 125
 Asn Glu Pro Thr Arg Leu Lys Gly Gln Ala Tyr Thr Ile Asp Asp Ala
 130 135 140
 Asp Pro Thr Gly Ser Gly Lys Trp Asn Phe Val Gly Thr Ile Asp Asn
 145 150 155 160

Asp Ala Thr Ile Val Glu Ile Arg Phe Leu Ala Arg Val Ala Ala Ala
 165 170 175
 Ala Thr Gly Pro Glu Gly Asp Val Tyr Arg Ala Ser Ala Thr Arg Gly
 180 185 190
 Ile Thr Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln
 195 200 205
 Val Trp Pro Leu Gln Gly Gly Tyr His Asp Ala Ile Thr Leu Asn Asp
 210 215 220
 Gly Ala Met Ile His Val Leu Glu Leu Phe Asp Asp Ile Ala Ser Gly
 225 230 235 240
 Gln Gly Asp Phe Ala Phe Leu Pro Glu Pro Leu Arg Asp Lys Val Glu
 245 250 255
 Ala Ala Gln Ala Lys Gly Gln Lys Val Leu Leu Asp Leu Gln Leu Lys
 260 265 270
 Arg Asn Gly Glu Arg Thr Leu Trp Ala Gln Gln Tyr Asp Pro Ile Thr
 275 280 285
 Leu Leu Pro Ser Ala Ala Arg Asn Tyr Glu Pro Ser Ser Ile Ser Thr
 290 295 300
 Gly Glu Ser Ala Gly Val Leu Ile Tyr Leu Met Ser Leu Pro Asn Pro
 305 310 315 320
 Ser Pro Glu Val Arg Asp Ala Ile Glu Lys Gly Val Ala Leu Leu Ile
 325 330 335
 Lys Leu Gln Ile Asn Gly Met Ala Trp Glu Lys Asp Gly Met Arg Lys
 340 345 350
 Arg Leu Val Ala Lys Ala Asp Ala Ser Pro Leu Trp Ser Arg Tyr His
 355 360 365
 Asp Ser Glu Thr Leu Leu Pro Ile Phe Gly Asp Arg Asp Met Arg Ile
 370 375 380
 Phe Asp Asp Val Asn Asp Ile Ser Asp Glu Arg Ser Arg Gly Tyr Ala
 385 390 395 400
 Trp Tyr Gly Thr Ser Pro Ala Arg Ala Ile Ala Glu Tyr Glu Lys Trp
 405 410 415
 Lys Gln Gly Asn Gly Lys
 420

<210> 23
 <211> 1182
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 23
 atgaaccgtg gcgtgattgt tttgctggcg gccgctccag ctgcggcgca tggcgcgagt
 60
 ctggggtata tgacgcctgc gcagccgttg accgagggcg gcattgccgc gctgccggcg
 120
 tcggagcagg gcgcctggcg gggctacctc gcccgctccc gcgcagccat ggacgccgac
 180
 aaggccgccc tggccgccga gcgcgccg cgccgaccg taccgccggc gccgccgcat
 240
 ggcggtggtg atggcgggat ggcgcgcaac cgtccgacgg cttggtatgg gacgccggaa
 300
 gcgcggcaca tcgcggacaa tatcgtcagc ttccagacgc cgtccggcgg ctggggcaag
 360
 aacgtggacc gcacgggacc tgtgcgccag cgcgacagc attacgtttc cttcgatggc
 420
 aaggagtcct ggaacttcat cggcacgac gacaacaacg ccacaacgag cgagctgaaa
 480
 ttcttgccgc gcgtgcaggc gcaaatgccc ggcgcggcgg gcgacgaata ccggaaggcc

540
 gccctgcgcg gcatcagcta cctgttgaac tcacaatatc ccaacggcgg cttcccgcag
 600
 gtctatccgc tgcaaggcgg ctaccacgac gccatcacct tcaacgacga tgccttcgcc
 660
 aacgtgctgc aagtgtgtct ggaagtggcg aaccgcaggg gcgactatgc cttcgtcccc
 720
 gaaaccgtgg caaccgatgc ccgcgcggcc gcggacaagg cgctccaagt cctgctggcg
 780
 agccagatca tcgtcggcgg cgtacgcacc gcctgggtgcc agcagcacga tgcgatcacg
 840
 ctggcgcccc tcggcgcccc caatttcgaa ccggccgcgc tgaccagcac ggaaagcgcg
 900
 cgctgtgctga tgctgttgat gctgctgccc gatccgagcc cggagctgag agcgtcaatc
 960
 catgcgggga tggcctggct gcagaaagcg gcgctgccgg gggatgtctg gtcgcgctac
 1020
 tatgacctga acacgatgag gccgatcttt ggggatcgtg accgcagtat ccacgatgat
 1080
 gtgaaggaat tgagcgagga gaggcaaaaa ggctatggct ggttcagtaa cggaccagcc
 1140
 agagctaaac aggcttttga ggcctggacg cgcaaacctt ga
 1182

<210> 24
 <211> 393
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN
 <222> (19)...(393)
 <223> Catalytic domain

<400> 24
 Met Asn Arg Gly Val Ile Val Leu Leu Ala Ala Ala Pro Ala Ala Ala
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 His Gly Ala Val Leu Gly Tyr Met Thr Pro Ala Gln Pro Leu Thr Glu
 20 25 30
 Ala Arg Ile Ala Ala Leu Pro Ala Ser Glu Gln Gly Ala Trp Arg Gly
 35 40 45
 Tyr Leu Ala Arg Ser Arg Ala Ala Met Asp Ala Asp Lys Ala Ala Leu
 50 55 60
 Ala Ala Glu Arg Ala Ala Leu Ala Thr Val Pro Pro Ala Pro Pro His
 65 70 75 80
 Gly Gly Gly Asp Gly Gly Met Ala Arg Asn Arg Pro Thr Ala Trp Tyr
 85 90 95
 Gly Thr Pro Glu Ala Arg His Ile Ala Asp Asn Ile Val Ser Phe Gln
 100 105 110
 Thr Pro Ser Gly Gly Trp Gly Lys Asn Val Asp Arg Thr Gly Pro Val
 115 120 125
 Arg Gln Arg Gly Gln His Tyr Val Ser Phe Asp Gly Lys Glu Ser Trp
 130 135 140
 Asn Phe Ile Gly Thr Ile Asp Asn Asn Ala Thr Thr Ser Glu Leu Lys
 145 150 155 160
 Phe Leu Ala Arg Val Gln Ala Gln Met Pro Gly Ala Ala Gly Asp Glu


```

tttgcatctcg tgaccaaagc gcagcaaatc gcagcgtcag ctagcctcgc gcgtgcactt
720
gattgcgtat tgaaatcaca agttgtcgtc aatggcacac gcacactctg gggcgcacag
780
cacgatgtta aaacactgca accaaccaaa gcgcgcgcat ttgaaatggt gtcactcact
840
accactgaaa gcgcagccat gctcagtttt ctgatggata tcaaaaatcc cagcgcggat
900
attattcaat ccatacatgc agccatagcc tggatatgagc aaaataaaaat cgctcggaata
960
acctggacac gtggtgatgc ggaattaaaa gataataaaa attcgcagcc actctgggag
1020
cgtttttatg agataggcac taataagcct atatttgggg atcgcgatga cactgtgtat
1080
tacgatttgg caaaagtgtc taaagagcgt cgcgaagggt atgctgggta ctccactgac
1140
ccgaataaga cgctaaaaaa atatgctgaa tgggtctaaaa aatatcccaa ataa
1194

```

```

<210> 26
<211> 397
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

```

```

<221> SIGNAL
<222> (1)...(15)

```

```

<221> DOMAIN
<222> (16)...(397)
<223> Catalytic domain

```

```

<400> 26
Met Val Ala Ala Leu Leu Ser Cys Gly Ser Ala Asn Leu Tyr Ala Glu
 1          5          10          15
Ser Thr Ala Lys Ser Val Thr Gln Ser Ala Ala Thr Asn Gln Leu Gln
 20          25          30
Asn Glu Lys Ser Ser Trp Asp Ser Tyr Tyr Ala Ala Ser Lys Lys Ile
 35          40          45
His Gln Ala Asp Gln Asp Phe Leu Ala Ala Glu Leu Lys Lys Leu Gly
 50          55          60
Gln Lys Lys Pro Thr Leu Pro Ala His Thr Lys Asp Phe Gly Phe Asp
 65          70          75          80
Val Lys Gln Val Asn Ala Asp Trp Phe Lys Ser Asp Glu Gly Lys Arg
 85          90          95
Val Met Glu Ile Ile Leu Ser Phe Gln Thr Pro Ser Gly Gly Trp Ser
100          105          110
Lys Arg Thr Asp Met Ala Lys Ala Val Arg Gln Pro Gly Gln Ala Phe
115          120          125
Gly Val Glu Lys Gly Tyr Ile Pro Thr Phe Asp Asn Gly Ala Thr Ser
130          135          140
Thr Gln Leu Met Leu Leu Ala Gln Ala His Gln Ala Thr Gly Asp His
145          150          155          160
Arg Phe Ser Asp Ala Phe Gly Arg Gly Leu Gln Leu Ile Leu Thr Ala
165          170          175
Gln Tyr Pro Asn Gly Gly Trp Pro Gln Asn Phe Pro Leu Thr Gly Ser
180          185          190
Tyr His Asp Tyr Ile Thr Tyr Asn Asp Asn Leu Thr Arg Asp Leu Met
195          200          205

```

Val	Val	Leu	His	Lys	Thr	Ala	Gln	Ala	Lys	Asn	Asp	Phe	Ala	Phe	Val
	210					215				220					
Thr	Lys	Ala	Gln	Gln	Ile	Ala	Ala	Ser	Ala	Ser	Leu	Ala	Arg	Ala	Leu
225					230					235					240
Asp	Cys	Val	Leu	Lys	Ser	Gln	Val	Val	Val	Asn	Gly	Thr	Arg	Thr	Leu
				245					250					255	
Trp	Gly	Ala	Gln	His	Asp	Val	Lys	Thr	Leu	Gln	Pro	Thr	Lys	Ala	Arg
			260					265					270		
Ala	Phe	Glu	Met	Val	Ser	Leu	Thr	Thr	Thr	Glu	Ser	Ala	Ala	Met	Leu
		275					280					285			
Ser	Phe	Leu	Met	Asp	Ile	Lys	Asn	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Ser
	290					295					300				
Ile	His	Ala	Ala	Ile	Ala	Trp	Tyr	Glu	Gln	Asn	Lys	Ile	Val	Gly	Lys
305					310					315					320
Thr	Trp	Thr	Arg	Gly	Asp	Ala	Glu	Leu	Lys	Asp	Asn	Lys	Asn	Ser	Gln
				325					330					335	
Pro	Leu	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Lys	Pro	Ile	Phe
			340					345					350		
Gly	Asp	Arg	Asp	Asp	Thr	Val	Tyr	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Lys
		355					360					365			
Glu	Arg	Arg	Glu	Gly	Tyr	Ala	Trp	Tyr	Ser	Thr	Asp	Pro	Asn	Lys	Thr
	370					375					380				
Leu	Lys	Lys	Tyr	Ala	Glu	Trp	Ser	Lys	Lys	Tyr	Pro	Lys			
385					390					395					

<210> 27
 <211> 1917
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 27
 gtgtctctct ttagaaaact cgcactgccg gttctgtgcg gtctactgct ttctgtcgga
 60
 gcagaaaccc gagcgctgaa gcgcattgtc gtggccgctg atggatcggg tgacgtcagg
 120
 acgattcaac aagcgggtgga ccagggtccc aaagacaata cacaccgggt cttgattcag
 180
 atcaagccgg gtgtgtatca ggaacaagtg cgtgtcgccg ccggcaaacg ctttatcact
 240
 cttcgcgggc acgacgcgag caagaccgtc atcacctatc gattgagcgc actacaagcg
 300
 ggaaataccc ggttggcatt caccacctta attaattgag acgactttcg cgccgagaac
 360
 ctgacgtttg aaaactcctt cggcaccggg tcacaagcgg ttgctttgtt tgtcgatgcg
 420
 aaccgcgcga cgtttgaaaa ctgccggttc ctcgggtggc aggacacttt gtttgtgaac
 480
 ggagccgcc acttcttcaa agactgctac gtcgaaggcc atgtcgattt cattttcggc
 540
 acggcctccg cagtgtttga gaactgcacc attcacagca aaggcgaagg ttatgtgacc
 600
 gcgcactatc gcaccagcga tgagatggat accggttttg tctttcatcg ttgtcgtttg
 660
 accggacgag acacggggccg cggagtttat ctcggaaggc cgtggcgacc ttacgcgcgc
 720
 gtcgtcttta tcgattgctg gctggacgca cacatcagac ctgaaggctg ggataattgg
 780
 agagatcctg aacgagagaa gaccgcgtgg tttgccgagt acaagtcaaa agggcccggt

840
 gctaatacccg tagctcgtgt cgcgtggtcc aggcagttga cgacagaaca agccgccgag
 900
 ttttcgcggg aacgcttttt cagccgcgct gttcgcgggc tctctgggca ggccaaccag
 960
 gcagtcggaa cgatcgcgtg ggacgatgcg cagaaaaaac cgaacgagtg gtatgcgagc
 1020
 gccgaggcgt tgcgcatcgc cgacaacggt gttctttatc aacgtgactc cggcggtcgg
 1080
 cccaagaaca tcgacatggg gaagccgctc gacgacaagg gtcgagccgg tcttctgcgc
 1140
 gtgcgtaaga agaacgattc caccatcgat aacggcgcga cttacacgca actctcgttt
 1200
 ctacgcgggg ttacacggc gcaaaagcag gagcggcatc gcgagtcgtt tctgaaggga
 1260
 ctcgattacc tgttgaaggc gcagtatcca aacggagggt ggccgcagtt ctatcccaat
 1320
 ctcaacggct attacaaaca catcactttc aacgacaacg cgatgatcgg cgtgatgaaa
 1380
 ctgctgcgcg acgtagcggc agcgaaccg gcgtatgcgt ttgtcgacga agcacgacga
 1440
 acgagtcgcg cgaaggcgggt cgaaaaagga atcgagtgcga tactgaagac gcaggtggtt
 1500
 gtgaatggcc ggcgaccgt gtggtgtgcg caacatgacg aagtcacgct cgcgcctgcc
 1560
 ccggcgagga cgtttgaatt agtttcgctg agtgggtgtg aaagcgttga gatcgtgcgc
 1620
 tttttgatgt cgatcaagaa cccgtcgccg gcggttgtcg aggcgatcga gtcggcggtt
 1680
 gcgtggttcg agcaatcgca agtgaaagat cccgccggca aacctgcgtg ggcgcgattt
 1740
 tatgagatcg gactaatcg tccgatcttc gccgggcgtg acggcgtcgt taagtatgat
 1800
 gtgaaacaga tcgatgagga acgacgaaag aattacgcat ggtacgttga cgacgcagcg
 1860
 aaactactga agaccgacta tcctgagtgg aaagaaaaga acgccaaga tcaatga
 1917

<210> 28
 <211> 638
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(638)
 <223> Catalytic domain

<400> 28
 Met Ser Leu Phe Arg Lys Leu Ala Leu Pro Val Leu Cys Gly Leu Leu
 1 5 10 15
 Leu Ser Val Gly Ala Glu Thr Arg Ala Ser Lys Arg Ile Val Val Ala

			20					25				30			
Ala	Asp	Gly	Ser	Gly	Asp	Val	Arg	Thr	Ile	Gln	Gln	Ala	Val	Asp	Gln
		35					40					45			
Val	Pro	Lys	Asp	Asn	Thr	His	Pro	Val	Leu	Ile	Gln	Ile	Lys	Pro	Gly
	50					55					60				
Val	Tyr	Gln	Glu	Gln	Val	Arg	Val	Ala	Ala	Gly	Lys	Arg	Phe	Ile	Thr
65					70					75				80	
Leu	Arg	Gly	Asp	Asp	Ala	Ser	Lys	Thr	Val	Ile	Thr	Tyr	Arg	Leu	Ser
				85					90					95	
Ala	Leu	Gln	Ala	Gly	Asn	Thr	Arg	Leu	Ala	Phe	Thr	Thr	Leu	Ile	Asn
			100					105					110		
Ala	Asp	Asp	Phe	Arg	Ala	Glu	Asn	Leu	Thr	Phe	Glu	Asn	Ser	Phe	Gly
		115					120					125			
Thr	Gly	Ser	Gln	Ala	Val	Ala	Leu	Phe	Val	Asp	Ala	Asn	Arg	Ala	Thr
	130					135					140				
Phe	Glu	Asn	Cys	Arg	Phe	Leu	Gly	Trp	Gln	Asp	Thr	Leu	Phe	Val	Asn
145					150					155					160
Gly	Ser	Arg	His	Phe	Phe	Lys	Asp	Cys	Tyr	Val	Glu	Gly	His	Val	Asp
				165					170					175	
Phe	Ile	Phe	Gly	Thr	Ala	Ser	Ala	Val	Phe	Glu	Asn	Cys	Thr	Ile	His
			180					185					190		
Ser	Lys	Gly	Glu	Gly	Tyr	Val	Thr	Ala	His	Tyr	Arg	Thr	Ser	Asp	Glu
		195					200					205			
Met	Asp	Thr	Gly	Phe	Val	Phe	His	Arg	Cys	Arg	Leu	Thr	Gly	Arg	Asp
	210					215					220				
Thr	Gly	Arg	Gly	Val	Tyr	Leu	Gly	Arg	Pro	Trp	Arg	Pro	Tyr	Ala	Arg
225					230					235					240
Val	Val	Phe	Ile	Asp	Cys	Trp	Leu	Asp	Ala	His	Ile	Arg	Pro	Glu	Gly
				245					250					255	
Trp	Asp	Asn	Trp	Arg	Asp	Pro	Glu	Arg	Glu	Lys	Thr	Ala	Trp	Phe	Ala
			260					265					270		
Glu	Tyr	Lys	Ser	Lys	Gly	Pro	Gly	Ala	Asn	Pro	Val	Ala	Arg	Val	Ala
		275					280					285			
Trp	Ser	Arg	Gln	Leu	Thr	Thr	Glu	Gln	Ala	Ala	Glu	Phe	Ser	Arg	Glu
	290					295					300				
Arg	Phe	Phe	Ser	Arg	Ala	Val	Arg	Gly	Leu	Ser	Gly	Gln	Ala	Asn	Gln
305					310					315					320
Ala	Val	Gly	Thr	Ile	Ala	Trp	Asp	Asp	Ala	Gln	Lys	Lys	Pro	Asn	Glu
				325					330					335	
Trp	Tyr	Ala	Ser	Ala	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Leu
			340					345					350		
Tyr	Gln	Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Gly	Lys
		355					360					365			
Pro	Leu	Asp	Asp	Lys	Gly	Arg	Ala	Gly	Leu	Leu	Arg	Val	Arg	Lys	Lys
	370														

Asp	Glu	Val	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Thr	Phe	Glu	Leu	Val
		515					520					525			
Ser	Leu	Ser	Gly	Gly	Glu	Ser	Val	Glu	Ile	Val	Arg	Phe	Leu	Met	Ser
	530					535					540				
Ile	Lys	Asn	Pro	Ser	Pro	Ala	Val	Val	Glu	Ala	Ile	Glu	Ser	Ala	Val
545					550				555						560
Ala	Trp	Phe	Glu	Gln	Ser	Gln	Val	Lys	Asp	Pro	Ala	Gly	Lys	Pro	Ala
			565						570						575
Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Ala	Gly
			580					585					590		
Arg	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Lys	Gln	Ile	Asp	Glu	Glu	Arg
		595					600					605			
Arg	Lys	Asn	Tyr	Ala	Trp	Tyr	Val	Asp	Asp	Ala	Ala	Lys	Leu	Leu	Lys
	610					615					620				
Thr	Asp	Tyr	Pro	Glu	Trp	Lys	Glu	Lys	Asn	Ala	Lys	Asp	Gln		
625					630					635					

<210> 29

<211> 1398

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 29

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atgattaacc gtcgagattt cataaaagac ctcattcatca cctccgccgg agtcgcggtt
60
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120
gcgcggatca aaccgccgaa atttccgaag cgcgatttcg tcatcacgaa gttcggcgcg
180
aaggcgggaa ccgatagcac gcaagcgatc gctaaagccc tcgacgcttg cgcgaaagcc
240
ggcgggcgac gcgtcgtcgt acccgccggc gaattttctca ccggtgcat ccattctcaag
300
tcgaacacca atctctacgt ctcaaaaggc gcgactctga agttttcgac cgaccccgaa
360
aaatatctgc cgatcgttca cacgcggttg gaagggatgg agttgatgca tctctcgccg
420
ttcatctacg cgtacgagca gacgaacatc gcgatcaccg gcgagggcac gctcgacggc
480
caaggcaaat cgttcttttg gaagtggcac ggcaaccgc gatacggcgg caaccccgaa
540
gtgatcagtc agcaaaaagc gcgggcgcga ctttacgaga tgatggacaa gaacgtaccc
600
gtcgcggagc gcgtgttcgg tatcgggcac tatctccggc cgagttcat ccagccgtac
660
aaatgtaaga acgtcttgat cgaaggcgtg acgatcatcg actcgccgat gtgggaagtt
720
catccggtgc tttgcgagaa tgtcaccgtc cgcaatcttc acatctcgtc gcacggtccg
780
aacaacgacg gctgcgatcc cgagtcgtgc aaagacgtcc tgatcgacaa ctgcttcttc
840
gacaccggtg acgactgcat cgcatcaag tcgggtcgca ataacgacgg tcgtcgtctg
900
aacacaccga ccgagaacat catcgtccgc aactgcacga tgaaagacgg tcacggtggt
960
atcacggtcg gaagcgagat ctcgggcggc gtgcgaaact tgttcgacac cgattgcaag
1020
atggacagtg cggatctgtg gaccgcgctc cgggtaaaga acaacgcatt gcggggcggc

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1080
 atgctggaga atttctatatt cgcgaacatc accgtcgggc aagtcgcgcg tgctgtggtc
 1140
 gagatcgatt tcaactatga agaaggcgcg aagggatcgt acacaccggt catgcgcaac
 1200
 tacgtgggtcg aggatctgac gtgcaccagc gggaaccggc ccgtcgatct gcaaggatta
 1260
 gacaacgcgc caatttacga tgtgtcgtg cgtaacacga ccttcggcgc gatgaagaac
 1320
 aagagcgtcg tgaagaatgt ccgaggactg aagatcgaaa acgttaccgt cagcggcacg
 1380
 cgcgtggaga gtttatga
 1398

<210> 30
 <211> 465
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(27)

<221> DOMAIN
 <222> (77)...(459)
 <223> Catalytic domain

<400> 30
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 1 5 10 15
 Gly Val Ala Val Leu Pro Gln Leu Ala Phe Gly Gln Asn Asp Pro Trp
 20 25 30
 Lys Thr Gln Tyr Pro Gln Ile Leu Ala Arg Ile Lys Pro Pro Lys Phe
 35 40 45
 Pro Lys Arg Asp Phe Val Ile Thr Lys Phe Gly Ala Lys Ala Gly Thr
 50 55 60
 Asp Ser Thr Gln Ala Ile Ala Lys Ala Leu Asp Ala Cys Ala Lys Ala
 65 70 75 80
 Gly Gly Gly Arg Val Val Pro Ala Gly Glu Phe Leu Thr Gly Ala
 85 90 95
 Ile His Leu Lys Ser Asn Thr Asn Leu Tyr Val Ser Lys Gly Ala Thr
 100 105 110
 Leu Lys Phe Ser Thr Asp Pro Glu Lys Tyr Leu Pro Ile Val His Thr
 115 120 125
 Arg Trp Glu Gly Met Glu Leu Met His Leu Ser Pro Phe Ile Tyr Ala
 130 135 140
 Tyr Glu Gln Thr Asn Ile Ala Ile Thr Gly Glu Gly Thr Leu Asp Gly
 145 150 155 160
 Gln Gly Lys Ser Phe Phe Trp Lys Trp His Gly Asn Pro Arg Tyr Gly
 165 170 175
 Gly Asn Pro Glu Val Ile Ser Gln Gln Lys Ala Arg Ala Arg Leu Tyr
 180 185 190
 Glu Met Met Asp Lys Asn Val Pro Val Ala Glu Arg Val Phe Gly Ile
 195 200 205
 Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro Tyr Lys Cys Lys Asn
 210 215 220
 Val Leu Ile Glu Gly Val Thr Ile Ile Asp Ser Pro Met Trp Glu Val
 225 230 235 240
 His Pro Val Leu Cys Glu Asn Val Thr Val Arg Asn Leu His Ile Ser

Ser His Gly Pro Asn Asn Asp Gly Cys Asp Pro Glu Ser Cys Lys Asp
 245 250 255
 Val Leu Ile Asp Asn Cys Phe Phe Asp Thr Gly Asp Asp Cys Ile Ala
 260 265 270
 Ile Lys Ser Gly Arg Asn Asn Asp Gly Arg Arg Leu Asn Thr Pro Thr
 275 280 285
 Glu Asn Ile Ile Val Arg Asn Cys Thr Met Lys Asp Gly His Gly Gly
 290 295 300 305 310 315 320
 Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val Arg Asn Leu Phe Ala
 325 330 335
 His Asp Cys Lys Met Asp Ser Ala Asp Leu Trp Thr Ala Leu Arg Val
 340 345 350
 Lys Asn Asn Ala Ser Arg Gly Gly Met Leu Glu Asn Phe Tyr Phe Arg
 355 360 365
 Asn Ile Thr Val Gly Gln Val Ala Arg Ala Val Val Glu Ile Asp Phe
 370 375 380
 Asn Tyr Glu Glu Gly Ala Lys Gly Ser Tyr Thr Pro Val Met Arg Asn
 385 390 395 400
 Tyr Val Val Glu Asp Leu Thr Cys Thr Ser Gly Asn Arg Pro Val Asp
 405 410 415
 Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp Val Ser Leu Arg Asn
 420 425 430
 Thr Thr Phe Gly Ala Met Lys Asn Lys Ser Val Val Lys Asn Val Arg
 435 440 445
 Gly Leu Lys Ile Glu Asn Val Thr Val Ser Gly Thr Arg Val Glu Ser
 450 455 460
 Leu
 465

<210> 31
 <211> 1401
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 31
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 acgccttcca ctgcggcgat tacggcggcc atcgaaaactt gtgccgcggc cgggggagga
 120
 gtggtctaca tcccggccgg acggttcctc accggtcccc tccgcctcaa aagccacgtc
 180
 cggctccatc tcgaggccgg agcgcacttg ctctttagtc aggaccggc cgattatcct
 240
 gttctggaga cgaggtggga ggggaaggag gtcttgacct atgcacacca gatctacggc
 300
 gaggacctcg aaggggtcgc gattaccggt cgggggacca tcgacggccg gggcgagact
 360
 tgggtggcgac tcttccgcgc caaagccttc acccatcccc gaccccgctt catcgccttt
 420
 accgctgca aggacatcct gatagaagga gtaaccctcg tcaattcacc ggcctggacc
 480
 atcaatcctg tgatgtgcga gcgggtgacc atcgataagg tgactatcat caaccgccc
 540
 gactcgcca acaccgacgg gatcgacccc gattcctccc ggaacgtcta tatcactaac
 600
 tgctacattg acgtaggcga tgactgcac gccatcaaa cggggccgaga ggactccctt
 660

tatcggacgc cttgtgaaaa cattgtcatc gccaaactgcc tcatgcgcca cggtcacggc
720
ggggtgggtca tcggcagcga gaccagcggg ggtattcgca aggtagtcac taccaactgc
780
atcttcgagg acaccgaccg gggcattaga cttaatcccc ggcgcgagc cggcgggttc
840
gtcaggagacc tccgggcgac gaattattatc atggaaaagg tgctctgtcc cttcgtcctc
900
aacatgtact atgataccgg gggaggcgtg atcgacgagc gcgcgcatga cttagaaccc
960
catccggtaa gcgaggctac accctccttc cgccgcctct ccttcagtca cattactgcc
1020
cgggaagtgc aggcgcgcgc ggccttcctc tacggcctgc ccgaacagcc tctggaggac
1080
gtcttatttg acgatatctg gatagagctg gccgcccagc cttctcctgc ccgtccggcc
1140
atgatgcggg ccgtcccgcc catgagccaa ggtggtgtgc tctgctacgg tgcgcggcgg
1200
atctccttcc ggcacatgca cctccgcggg caccgcggtc cggccttcca gatcgaacgc
1260
gcggaggcgg tgcagttgat gggctgctcg accgacggca gtgaagaccc ccagcttgtc
1320
ttgggtcaag cggaggaggt caccatccgt gactgcacct ttaccgcca gcaggacccc
1380
gcaaaaagaaa ggcaaaatta a
1401

<210> 32
<211> 466
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(348)
<223> Catalytic domain

<400> 32
Met Ile Asn Leu Tyr Gly Val Phe Asp Ile Arg Thr Phe Gly Ala Gln
1 5 10 15
Pro Asp Gly Glu Thr Pro Ser Thr Ala Ala Ile Thr Ala Ala Ile Glu
20 25 30
Thr Cys Ala Ala Ala Gly Gly Gly Val Val Tyr Ile Pro Ala Gly Arg
35 40 45
Phe Leu Thr Gly Pro Leu Arg Leu Lys Ser His Val Arg Leu His Leu
50 55 60
Glu Ala Gly Ala His Leu Leu Phe Ser Gln Asp Pro Ala Asp Tyr Pro
65 70 75 80
Val Leu Glu Thr Arg Trp Glu Gly Lys Glu Val Leu Thr Tyr Ala His
85 90 95
Gln Ile Tyr Gly Glu Asp Leu Glu Gly Val Ala Ile Thr Gly Arg Gly
100 105 110
Thr Ile Asp Gly Arg Gly Glu Thr Trp Trp Arg Leu Phe Arg Ala Lys
115 120 125
Ala Phe Thr His Pro Arg Pro Arg Leu Ile Ala Phe Thr Arg Cys Lys
130 135 140
Asp Ile Leu Ile Glu Gly Val Thr Leu Val Asn Ser Pro Ala Trp Thr
145 150 155 160
Ile Asn Pro Val Met Cys Glu Arg Val Thr Ile Asp Lys Val Thr Ile

Ile	Asn	Pro	Pro	Asp	Ser	Pro	Asn	Thr	Asp	Gly	Ile	Asp	Pro	Asp	Ser
			180						185				190		
Ser	Arg	Asn	Val	Tyr	Ile	Thr	Asn	Cys	Tyr	Ile	Asp	Val	Gly	Asp	Asp
		195					200					205			
Cys	Ile	Ala	Ile	Lys	Ala	Gly	Arg	Glu	Asp	Ser	Leu	Tyr	Arg	Thr	Pro
	210					215					220				
Cys	Glu	Asn	Ile	Val	Ile	Ala	Asn	Cys	Leu	Met	Arg	His	Gly	His	Gly
225					230					235				240	
Gly	Val	Val	Ile	Gly	Ser	Glu	Thr	Ser	Gly	Gly	Ile	Arg	Lys	Val	Val
				245						250				255	
Ile	Thr	Asn	Cys	Ile	Phe	Glu	Asp	Thr	Asp	Arg	Gly	Ile	Arg	Leu	Lys
			260					265					270		
Ser	Arg	Arg	Gly	Arg	Gly	Gly	Phe	Val	Glu	Asp	Leu	Arg	Ala	Thr	Asn
		275					280					285			
Ile	Ile	Met	Glu	Lys	Val	Leu	Cys	Pro	Phe	Val	Leu	Asn	Met	Tyr	Tyr
	290					295					300				
Asp	Thr	Gly	Gly	Gly	Val	Ile	Asp	Glu	Arg	Ala	His	Asp	Leu	Glu	Pro
305					310					315				320	
His	Pro	Val	Ser	Glu	Ala	Thr	Pro	Ser	Phe	Arg	Arg	Leu	Ser	Phe	Ser
				325					330					335	
His	Ile	Thr	Ala	Arg	Glu	Val	Gln	Ala	Ala	Ala	Ala	Phe	Leu	Tyr	Gly
			340					345					350		
Leu	Pro	Glu	Gln	Pro	Leu	Glu	Asp	Val	Leu	Phe	Asp	Asp	Ile	Trp	Ile
		355					360					365			
Glu	Leu	Ala	Ala	Asp	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Met	Met	Arg	Ala
	370					375					380				
Val	Pro	Pro	Met	Ser	Gln	Gly	Gly	Val	Leu	Cys	Tyr	Gly	Ala	Arg	Arg
385					390					395				400	
Ile	Ser	Phe	Arg	His	Met	His	Leu	Arg	Gly	His	Arg	Gly	Pro	Ala	Phe
				405					410					415	
Gln	Ile	Glu	Arg	Ala	Glu	Ala	Val	Gln	Leu	Met	Gly	Cys	Ser	Thr	Asp
			420					425					430		
Gly	Ser	Glu	Asp	Pro	Gln	Leu	Val	Leu	Gly	Gln	Ala	Glu	Glu	Val	Thr
		435					440				445				
Ile	Arg	Asp	Cys	Thr	Phe	Thr	Ala	Gln	Gln	Asp	Pro	Ala	Lys	Glu	Arg
	450					455					460				
Gln	Asn														
465															

<210> 33
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 33
 atgaaacttc gatgtctgat gctcaccctg cttcttttgcg gcagcgcctt cgccgccgac
 60
 cggattacgg ccgacaagat caacaacaag cccgactcct ggcttaccag cgacgaaggc
 120
 atcaagctga tcgacaacat catcacctgg cagaacccccg aggggtggctg ggccaagtac
 180
 tacgacgcga ccaatccgca caaacaaggc gaagtctacg gcgactggga cggcgctcggc
 240
 accatcgaca acggctacac ctacaccgag ctgaatctcc tggcgcacgt ctacaccctc
 300
 accaagcgcc cggagatcct cgattcgttc aacaagggcc tggagtttct gctcaaagcc
 360

caatacccca gcggcggtg gccgcaacgg tttccggtgc ccaacaacta cggcaagtgc
 420
 atcacgctca acgacaacgc gatggtgaac gtgatgcagt tcctgcagaa cgctgcaaag
 480
 ggcaaggaag acttcgcttt cgctgacgag cagcgctcgcg ccaaagcgaa ggaggcgttt
 540
 gaccgcggga tcgactgcct tctgaagctc cagattaccg tgaacggcaa gcttaccgcc
 600
 tgggccagc agtatgacct gaagacactc gccgcggcgc ccgcccgggc gtacgagctc
 660
 ccgggcctca gcggctgcga aagcgcgccc gtcatgcgct tgttcatgtc tttggagaac
 720
 cccagtcccg aagttcagcg cgccgtccac gcggcgggcg cttggtacga ggcgtcgaag
 780
 atcacgggca agaagctggg gcgcgagaac aacgacgtga cactggccga cgaccccaac
 840
 ggcgagccgc tttgggcgcg cttctacgac atcgaaacca accgcccgtt ctattgcggt
 900
 cgcgacggcg tgaagaagtg gtcgctggac gagatcgagc ccgaacgccg caagggctac
 960
 gcttgggtcc gcccctgggc gacgagcgta ctggagcagt atcgcaagtg ggcggcgaag
 1020
 caccacccg tgaacagttg a
 1041

<210> 34
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN
 <222> (19)...(346)
 <223> Catalytic domain

<400> 34
 Met Lys Leu Arg Cys Leu Met Leu Thr Leu Leu Leu Cys Gly Ser Ala
 1 5 10 15
 Phe Ala Ala Asp Arg Ile Thr Ala Asp Lys Ile Asn Asn Lys Pro Asp
 20 25 30
 Ser Trp Leu Thr Ser Asp Glu Gly Ile Lys Leu Ile Asp Asn Ile Ile
 35 40 45
 Thr Trp Gln Asn Pro Glu Gly Gly Trp Ala Lys Tyr Tyr Asp Ala Thr
 50 55 60
 Asn Pro His Lys Gln Gly Glu Val Tyr Gly Asp Trp Asp Gly Val Gly
 65 70 75 80
 Thr Ile Asp Asn Gly Tyr Thr Tyr Thr Glu Leu Asn Leu Leu Ala His
 85 90 95
 Val Tyr Thr Leu Thr Lys Arg Pro Glu Ile Leu Asp Ser Phe Asn Lys
 100 105 110
 Gly Leu Glu Phe Leu Leu Lys Ala Gln Tyr Pro Ser Gly Gly Trp Pro
 115 120 125
 Gln Arg Phe Pro Val Pro Asn Asn Tyr Gly Lys Cys Ile Thr Leu Asn
 130 135 140
 Asp Asn Ala Met Val Asn Val Met Gln Phe Leu Gln Asn Val Ala Lys
 145 150 155 160

840
ggcgagaaca cggttgtgaa agacaaatcg gctcccccta tatgggcacg gttctatcag
900
atcgaaacga tgcgtccgat cttcatcggg cgtgattcgg ttatcaagta tgacgtgacg
960
caggtcgaag ccgagcgtcg gaatgggttac gcctggtacg tcaccgcacc gaatgaattg
1020
gtgaacgagg attatttgaa gtggaagggg aaaagcgccg gagccaagta g
1071

<210> 36
<211> 356
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(356)
<223> Catalytic domain

<400> 36
Met Pro Lys Asn Ser Asp Asp Ala Trp Arg Glu Lys Thr Pro Pro Asp
1 5 10 15
Trp Ser Leu Val Thr Trp Ser Asp Val Phe Lys Gln Lys Pro Leu Trp
20 25 30
Tyr Gln Thr Asp Glu Ala Ala Arg Val Ala Asp Gln Leu Leu Ile Tyr
35 40 45
Gln Lys Glu Asn Gly Gly Phe Glu Lys Asn Val Asp Met Ala Leu Met
50 55 60
Leu Thr Gln Lys Glu Lys Glu Glu Leu Thr Ala Lys Arg Ser Asp Val
65 70 75 80
Ser Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Pro Gln Val Ala Tyr
85 90 95
Leu Gly Arg Val Ile Thr Ala Ser Leu Leu Lys Pro Ser Pro Pro Ala
100 105 110
Asn Leu Pro Lys Tyr Lys Asp Ala Phe Asn Lys Gly Leu Asp Tyr Leu
115 120 125
Leu Ala Ser Gln Tyr Glu Asn Gly Gly Phe Pro Gln Phe Tyr Pro Leu
130 135 140
Lys Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile
145 150 155 160
Gly Val Leu Lys Val Leu Arg Asp Ile Ala Asn Lys Lys Glu Asp Tyr
165 170 175
Val Phe Val Asp Glu Ala Arg Arg Leu Arg Ala Glu Gln Ala Val Ala
180 185 190
Lys Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Val Val Asp Gly Lys
195 200 205
Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Thr Thr Leu Ala Pro Ala
210 215 220
Ala Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val
225 230 235 240
Gly Ile Val Arg Tyr Leu Met Gln Glu Lys Pro Thr Pro Glu Ile Thr
245 250 255
Asp Ala Ile Glu Ser Ala Ile Asp Trp Tyr Arg Lys Asn Lys Ile Asp
260 265 270
Gly Ile Arg Trp Glu Arg Ile Lys Gly Glu Asn Thr Val Val Lys Asp
275 280 285
Lys Ser Ala Pro Pro Ile Trp Ala Arg Phe Tyr Gln Ile Glu Thr Met
290 295 300

Arg	Pro	Ile	Phe	Ile	Gly	Arg	Asp	Ser	Val	Ile	Lys	Tyr	Asp	Val	Thr
305					310					315					320
Gln	Val	Glu	Ala	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Tyr	Val	Thr	Ala
				325					330						335
Pro	Asn	Glu	Leu	Val	Asn	Glu	Asp	Tyr	Leu	Lys	Trp	Lys	Gly	Lys	Ser
			340					345					350		
Ala	Gly	Ala	Lys												
			355												

<210> 37
 <211> 1860
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 37
 atgttcacta ctactggctc tcattgcgcc cggaattccg cgcgtttttc ccttactgcg
 60
 atagcagccg ctgttgcgtt gatggcaggc acttcagcat ttgcagctgc gacgggtggc
 120
 ttctctacca ctgatggtgg caacgtatcg ggcgcccgtt cgtttactgc atcgacttac
 180
 cagcaaatca acaccattat tgccaacgca aaactggatg atgcaggtaa aaaagtcact
 240
 ggggggtgctt acccgcttat cattacctac accggtaatg aagactcgct gattaaccag
 300
 atgatcaaag accacacggt gaattcatcg ggcaactgcc ctaaccgcg ttggagcgaa
 360
 gcctatcgct acgtggaaat taaagagttt accaagggtta ttaccattca aggcgcgaat
 420
 ggttcttcag caaacttcgg cattgtgatt aataaatctg acaatgtgat tgtgcgtaat
 480
 atgaaaatcg gtgcgcttgc tgggtgcgagt aacgatgcgg atatgattcg tatcgacacc
 540
 ggcgttaacg tgtggattga tcacaacgaa ttgtttgcgg taaataatga atgtaaaggt
 600
 tcacccgatg gtgacctgac atttgaaagt gcgattgata ttaaaaaagc atcgcaaaat
 660
 attacggtgt cctacaacat tatccgcgat agtaaaaaag tagggctcga tggttcgagt
 720
 agcagtgata ttgcaggtgg ccgtaagatt acgttccatc acaatattta tcgcaatggt
 780
 ggtgcacgtt taccgttgca acgcggtggt tggacacaca tgtataacaa tctttacgac
 840
 ggagttacca gtcgggtat taacgttcgt caaggtggct acgcgctaata cgagaacaac
 900
 tggttccaaa atgctgtcaa cccggttacc tgccgttttg acagtagtaa ctgcggttac
 960
 tgggatctgc gcaacaacaa cgtgcgcaac cctggtgatt tctccaccta caacattacc
 1020
 tggaccagcg gtggcaccat cgacgccacc aactggacta ccactcaacc tttcccgatt
 1080
 agcattcctt acagctactc gcctgttagc ccgcagtgtg tcaaagacaa gttggcaaat
 1140
 tatgtctggtg tcggtaaaaa caatgcgcaa ttaacggcgt ctgcgtgcag cggaataact
 1200
 tcatcggtag caccttcacg agtgccagca tcatcggcgg caccttcaag ccgttcaccc
 1260
 agcagtgcag cgccatccag cacaccaact acatcaagct cgagttcagt tgccgcaacc

1320
 gggtcaattt cgctcgggtgc aacggcaacc aacaacagca ttgtgttgag ttggtcaccc
 1380
 aacaatgtga cgctcgggttc gcaagaagtg tatcgcgata ccgacgctga tccatcgggg
 1440
 cgtgtgcgta tcgcatccct ggctgcttca gcgcgtatgt ataccgatag cacagcggca
 1500
 tcggggccaaa cctattacta ctggattaaa aataccactt ctggtgttgt caccaattcc
 1560
 aatgctgcat cagcgcgtat tggtagcacg gcgtccagtt ctgttgcata aagcagctca
 1620
 agttcaagcg gcggcgcgcc cgtattaggt ggtactgggtg attatccaag cggcttctcc
 1680
 aagtgcgctg atttgggcgg gacttgttca gtgtcatcgg gcgatggctg gggtgcgttt
 1740
 ggtcgcaaaag gcaagtgggt taccaagaaa gtatcggtag gtagttcaat cgcctgtacc
 1800
 gttgcggcat ttggttcgga tccacagggc aaccctaaca agtgttctta caaacgttaa
 1860

<210> 38
 <211> 619
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(35)

<221> DOMAIN
 <222> (36)...(387)
 <223> Catalytic domain

<400> 38
 Met Phe Thr Thr Thr Gly Ser His Cys Ala Arg Asn Ser Ala Arg Phe
 1 5 10 15
 Ser Leu Thr Ala Ile Ala Ala Val Ala Leu Met Ala Gly Thr Ser
 20 25 30
 Ala Phe Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
 35 40 45
 Val Ser Gly Ala Arg Ser Phe Thr Ala Ser Thr Tyr Gln Gln Ile Asn
 50 55 60
 Thr Ile Ile Ala Asn Ala Lys Leu Asp Asp Ala Gly Lys Lys Val Thr
 65 70 75 80
 Gly Gly Ala Tyr Pro Leu Ile Ile Thr Tyr Thr Gly Asn Glu Asp Ser
 85 90 95
 Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asn Ser Ser Gly Asn
 100 105 110
 Cys Pro Asn Pro Arg Trp Ser Glu Ala Tyr Arg Tyr Val Glu Ile Lys
 115 120 125
 Glu Phe Thr Lys Gly Ile Thr Ile Gln Gly Ala Asn Gly Ser Ser Ala
 130 135 140
 Asn Phe Gly Ile Val Ile Asn Lys Ser Asp Asn Val Ile Val Arg Asn
 145 150 155 160
 Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp Ala Asp Met Ile
 165 170 175
 Arg Ile Asp Thr Gly Val Asn Val Trp Ile Asp His Asn Glu Leu Phe
 180 185 190
 Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly Asp Leu Thr Phe

	195		200		205
Glu	Ser	Ala	Ile	Asp	Ile
	210		215		220
Tyr	Asn	Ile	Ile	Arg	Asp
225			230		235
Ser	Ser	Asp	Ile	Ala	Gly
			245		250
Tyr	Arg	Asn	Val	Gly	Ala
			260		265
His	Met	Tyr	Asn	Asn	Leu
			275		280
Val	Arg	Gln	Gly	Gly	Tyr
			290		295
Ala	Val	Asn	Pro	Val	Thr
305				310	
Trp	Asp	Leu	Arg	Asn	Asn
				325	
Tyr	Asn	Ile	Thr	Trp	Thr
			340		345
Thr	Thr	Thr	Gln	Pro	Phe
			355		360
Val	Ser	Pro	Gln	Cys	Val
				370	
Gly	Lys	Asn	Asn	Ala	Gln
385				390	
Ser	Ser	Val	Ala	Pro	Ser
				405	
Ser	Arg	Ser	Ser	Ser	Ser
				420	
Ser	Ser	Ser	Ser	Val	Ala
				435	
Ala	Thr	Asn	Asn	Ser	Ile
				450	
Leu	Gly	Ser	Gln	Glu	Val
465				470	
Arg	Val	Arg	Ile	Ala	Ser
				485	
Ser	Thr	Ala	Ala	Ser	Gly
				500	
Thr	Ser	Gly	Val	Val	Thr
				515	
Ser	Thr	Ala	Ser	Ser	Ser
				530	
Gly	Ala	Pro	Val	Leu	Gly
545				550	
Lys	Cys	Ala	Asp	Leu	Gly
				565	
Trp	Val	Ala	Phe	Gly	Arg
				580	
Val	Gly	Ser	Ser	Ile	Ala
				595	
Gln	Gly	Asn	Pro	Asn	Lys
				610	
					615

<210> 39
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 39
atggcgccga tcctccgacc caacctcctt tgcacttacg cgctctgcat gggcttgctc
60
gccgtggtga gctgcgcggc ggggccggtg tcagcgcagc agccggcgcc atggagcacg
120
gccatcgtgg agcaggagga gagcgcgttc gcctccccgt cgatgcgcag cgtcgccgac
180
aacgtcgtgc gccatcagtc ggccgaaggc ggctggccta agaacaccaa tctggcgggc
240
ccgccatcgg ggccggcgcc ggagggcgtc gccaatacga tcgacaatga tgcgacgacg
300
ctgccgatgg agtttctggc gcgtgtgac caccggcgcg gcgtccgata caagccggcc
360
ttcgagcgcg ggctggatta tctgcttgcg gctcagtacg cgaacggcgg ctggccgcag
420
ttctatccgc tgcgcggggg ctattacgat cactgtgacgt tcaacgacga cgccatgatc
480
cgggtgatga ttctgctcgg cgcagtggcg cgcggcgggg cgccctatga atttgtcgac
540
gccggggcggc gcgcgcgcgc tgcagccgcg gtcgagcggg gcctggcgct catcctgcgc
600
acgcagatcc ggccggcgcg ggcgctgacg gtctggtgcg cgcagtatga cagcgccacc
660
ttgcagcccg cctgggcgcg cgcctatgag ccgccgtccc tgtccggcgc ggaaagtgtg
720
gggatcgtgc gctatctcat gtcgatcgac catccctcgc ccgaagtcgt cgccgccgtc
780
gacggcgctg tggcatggct gcgcgcggcc gccattgccg gcgtgcgcgt ggagaatttc
840
acggacgccg acggccgccc tgaccgccgc gccgtggccg acgcgggcgc gccgccgatc
900
tgggcgcggt tctacgagtt cggcgccaac cggccgatct tcctggggcg tgattccgtt
960
tttactaca cgttcgagga aatcgagcgc gagcggcgcg caggctacaa ttattacgga
1020
tactgggcgc gctccgtgct ggaagactat ccggcctggc gcgcgcgcgt gcgatga
1077

<210> 40
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(358)
<223> Catalytic domain

<400> 40
Met Ala Pro Ile Leu Arg Pro Asn Leu Leu Cys Thr Tyr Ala Leu Cys
1 5 10 15
Met Gly Leu Leu Ala Val Val Ser Cys Ala Ala Gly Pro Val Ser Ala
20 25 30
Gln Gln Pro Ala Pro Trp Ser Thr Ala Ile Val Glu Gln Glu Glu Ser
35 40 45

Ala	Phe	Ala	Ser	Pro	Ser	Met	Arg	Ser	Val	Ala	Asp	Asn	Val	Val	Arg
50						55					60				
His	Gln	Ser	Ala	Glu	Gly	Gly	Trp	Pro	Lys	Asn	Thr	Asn	Leu	Ala	Ala
65					70					75					80
Pro	Pro	Ser	Gly	Pro	Ala	Pro	Glu	Gly	Val	Ala	Asn	Thr	Ile	Asp	Asn
				85					90					95	
Asp	Ala	Thr	Thr	Leu	Pro	Met	Glu	Phe	Leu	Ala	Arg	Val	Ile	His	Ala
			100					105					110		
Gly	Gly	Val	Arg	Tyr	Lys	Pro	Ala	Phe	Glu	Arg	Gly	Leu	Asp	Tyr	Leu
		115					120					125			
Leu	Ala	Ala	Gln	Tyr	Ala	Asn	Gly	Gly	Trp	Pro	Gln	Phe	Tyr	Pro	Leu
	130					135					140				
Arg	Gly	Gly	Tyr	Tyr	Asp	His	Val	Thr	Phe	Asn	Asp	Asp	Ala	Met	Ile
145					150					155					160
Arg	Val	Met	Ile	Leu	Gly	Ala	Val	Ala	Arg	Gly	Gly	Ala	Pro	Tyr	
				165				170						175	
Glu	Phe	Val	Asp	Ala	Gly	Arg	Arg	Ala	Arg	Ala	Ala	Ala	Ala	Val	Glu
			180					185					190		
Arg	Gly	Leu	Ala	Leu	Ile	Leu	Arg	Thr	Gln	Ile	Arg	Gln	Gly	Gly	Ala
		195					200					205			
Leu	Thr	Val	Trp	Cys	Ala	Gln	Tyr	Asp	Ser	Ala	Thr	Leu	Gln	Pro	Ala
	210					215					220				
Trp	Ala	Arg	Ala	Tyr	Glu	Pro	Pro	Ser	Leu	Ser	Gly	Ala	Glu	Ser	Val
225					230					235					240
Gly	Ile	Val	Arg	Tyr	Leu	Met	Ser	Ile	Asp	His	Pro	Ser	Pro	Glu	Val
				245					250					255	
Val	Ala	Ala	Val	Asp	Gly	Ala	Val	Ala	Trp	Leu	Arg	Ala	Ala	Ala	Ile
			260					265					270		
Ala	Gly	Val	Arg	Val	Glu	Asn	Phe	Thr	Asp	Ala	Asp	Gly	Arg	Pro	Asp
		275					280					285			
Arg	Arg	Ala	Val	Ala	Asp	Ala	Gly	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe
	290					295					300				
Tyr	Glu	Phe	Gly	Ala	Asn	Arg	Pro	Ile	Phe	Leu	Gly	Arg	Asp	Ser	Val
305					310					315					320
Phe	His	Tyr	Thr	Phe	Gly	Glu	Ile	Glu	Arg	Glu	Arg	Arg	Ala	Gly	Tyr
				325					330					335	
Asn	Tyr	Tyr	Gly	Tyr	Trp	Ala	Arg	Ser	Val	Leu	Glu	Asp	Tyr	Pro	Ala
			340					345					350		
Trp	Arg	Ala	Arg	Val	Arg										
			355												

<210> 41
 <211> 1080
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 41
 atgaaaaaatt taaaatacag tttagtttca tttgtactac tcattactat gaatgttttt
 60
 acgcaagaaa aaaaagtaac ttggaaaagc atcacagaaa ataacgatga aaattgggtt
 120
 gtaagcgaag aagccaaaaa aatagccgaa aatgttttgt tatatcaacg cgatattggt
 180
 ggttggccaa aaaacactga aattcaaaat gaactttcag aaaaagaaaa actaacatta
 240
 aaagaattaa aatcggatcc aaaaggatgt accatcgaca atgggtgcaac gtgtcaggaa
 300
 ttacttttct tatccaaaat atataaatcc aatccagatg agcgatataa aatggctttc

360
 ttaaaagggtg tgatttacct gattacagct caatacaaaa atggtggttg gccacaatat
 420
 taccctttga gagaaggata ttacactcat attacttaca acgataatgc aatggtgaat
 480
 gttttaaaagt tggtgaaaga agttaaaagat aaatctgatt actactcaat tcaagcaccc
 540
 gatgaaatgtt ccaaaatggc tgaagtatca ttaataaaag gagtcgattg catattaaaa
 600
 acacagtaca aacaaaaatgg aatattaacc gcttggtgtg cacaacatga cagggaaca
 660
 ttgaaacctg ctaaagcaag agcttatgaa ttgccttcgt taagcggaaa agaatacagcc
 720
 aaaattgtgt tggtattaat gtcaatcgaa aatccatcta aagaagtaat tactgccgta
 780
 aattcagcag ttaattggtt tgaaaaaaca aaaatcaacg gaattaaaat tgaaaccatt
 840
 tccaccggga aaaaggatga aaaagataga attgttgttg aaagtcctga tgctccgccg
 900
 ctttgggcaa gatttatgga attaagtac aacaaacat tttttgtga tcgtgacgga
 960
 aagaaaaaat acagcatgtc agaaattagt caagagcgta gaaccggcta tgcattgtac
 1020
 accaacgaac caaaagaagt tttaaaaaaa tacgatgatt ggaagtcac attaaactaa
 1080

<210> 42
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(359)
 <223> Catalytic domain

<400> 42
 Met Lys Asn Leu Lys Tyr Ser Leu Val Ser Phe Val Leu Leu Ile Thr
 1 5 10 15
 Met Asn Val Phe Thr Gln Glu Lys Lys Val Thr Trp Lys Ser Ile Thr
 20 25 30
 Glu Asn Asn Asp Glu Asn Trp Phe Val Ser Glu Glu Ala Lys Lys Ile
 35 40 45
 Ala Glu Asn Val Leu Leu Tyr Gln Arg Asp Ile Gly Gly Trp Pro Lys
 50 55 60
 Asn Thr Glu Ile Gln Asn Glu Leu Ser Glu Lys Glu Lys Leu Thr Leu
 65 70 75 80
 Lys Glu Leu Lys Ser Asp Pro Lys Gly Cys Thr Ile Asp Asn Gly Ala
 85 90 95
 Thr Cys Gln Glu Leu Leu Phe Leu Ser Lys Ile Tyr Lys Ser Asn Pro
 100 105 110
 Asp Glu Arg Tyr Lys Met Ala Phe Leu Lys Gly Val Ile Tyr Leu Ile
 115 120 125
 Thr Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Leu Arg
 130 135 140
 Glu Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn

145					150					155				160
Val	Leu	Lys	Leu	Leu	Lys	Glu	Val	Lys	Asp	Lys	Ser	Asp	Tyr	Tyr
				165					170					175
Ile	Gln	Ala	Pro	Asp	Glu	Ile	Ser	Lys	Met	Ala	Glu	Val	Ser	Phe
			180					185					190	Asn
Lys	Gly	Val	Asp	Cys	Ile	Leu	Lys	Thr	Gln	Tyr	Lys	Gln	Asn	Gly
		195					200					205		Ile
Leu	Thr	Ala	Trp	Cys	Ala	Gln	His	Asp	Arg	Glu	Thr	Leu	Lys	Pro
	210					215					220			Ala
Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Ser	Leu	Ser	Gly	Lys	Glu	Ser
225					230					235				240
Lys	Ile	Val	Leu	Leu	Leu	Met	Ser	Ile	Glu	Asn	Pro	Ser	Lys	Glu
			245						250				255	Val
Ile	Thr	Ala	Val	Asn	Ser	Ala	Val	Asn	Trp	Phe	Glu	Lys	Thr	Lys
			260					265					270	Ile
Asn	Gly	Ile	Lys	Ile	Glu	Thr	Ile	Ser	Thr	Gly	Lys	Lys	Asp	Glu
	275						280					285		Lys
Asp	Arg	Ile	Val	Val	Glu	Ser	Pro	Asp	Ala	Pro	Pro	Leu	Trp	Ala
	290					295				300				Arg
Phe	Met	Glu	Leu	Ser	Asp	Asn	Lys	Pro	Phe	Phe	Cys	Asp	Arg	Asp
305					310					315				Gly
Lys	Lys	Lys	Tyr	Ser	Met	Ser	Glu	Ile	Ser	Gln	Glu	Arg	Arg	Thr
				325					330					Gly
Tyr	Ala	Trp	Tyr	Thr	Asn	Glu	Pro	Lys	Glu	Val	Leu	Lys	Lys	Tyr
			340					345					350	Asp
Asp	Trp	Lys	Ser	Ser	Leu	Asn								
		355												

<210> 43
 <211> 1902
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 43
 gtggatccaa agaattgggg cagcggattt accggcgaaa tcaaagtaac taacaacaca
 60
 agccaaacag tcaatagctg gtctgtgtca tggcaagagg caggagccag tgtaactaat
 120
 tcctggaatg caaccttggg agggacgaat ccttataaccg caaccggggtt aggatggaac
 180
 tcaaccctgg cgcccggagc ctctgccagt tttggttttc aagcaaacgg cactgcgggg
 240
 gcaccaaagg taaatggcag tttgtgtggt gcgactgcat catctgcagc gaccagcaaa
 300
 tccagtgcga gtgttgcgag ttcaaagatt gcaagttcaa ttcaatcaag tgcaactagc
 360
 agttcaaaat cgtccagttc tgctgcacct tcaagcacgc caaaatccag tagctctgct
 420
 ccaacggctg catcattcac tattcaagaa gagcaagccg gtttttgccg tgtagacggt
 480
 attgcaacgg aaagtaccaa caccggattc accggcaacg gctacaccaa ttccaataat
 540
 gtacaagggtg ctgccattgt gtgggcggtg aatgcaacta ccagtgcacg ccatacaatt
 600
 actttccgct tcgctaattg tggcactgct aatcgcaatg gctcgctagt cattaacggc
 660
 ggcagcaatg gtaattacac ggtgcaatta ccacgcaccg cgagctgggc tgactggcaa
 720

acagtaagtc tggaaattga tttggtacaa ggcaataaca atttgcaact caccgcattg
 780
 actgcagatg gcctcgcaaa tatcgacttc atcaaaattg aaggagcatc aaccaaagcg
 840
 ggaacctgtg caggtgcggt cagcagtagc agtgttgcct cttcggtaaa atccagtgt
 900
 agcgcggcaa gcagttctgt accaacgaac accggcgcca tgctaacttt ggatggcaac
 960
 cctgccgcaa gctggcttaa caaatcgctg acaaagtgga gcgcatcgcg cgctgacatt
 1020
 gttgcctctt atcaacagtc caacggcggc tggccaaaaa atctggatta caattcagt
 1080
 agcgtggta atggcggcag tgcaagcggc accatcgata atggtgcaac tattactgaa
 1140
 atggtttatc tcgctgaggt ttacaaaacc ggaaacaata ccaagtaccg cgatgcagtt
 1200
 cgccgtgcag caaactttat cgtgagttcg caatatagca ctggcgcggt gccgcaattt
 1260
 tatccgctca aaggtggcta tgcagaccac gccaccttta atgataacgg catggcttac
 1320
 gcattaactg tattggattt cgctgcaaac aagcgcgcgc cttttgatac ggatgtcttt
 1380
 aatgacacag accgcgcaaa atttaaaaca gcggtaacca aaggtgttga ttacatttta
 1440
 aaagcgcaat ggaaacaaaa tggaaaatta acagcctggt gcgcacaaca tggcgcgact
 1500
 gactatcaac ctaaaaaagc acgcgcttat gaattggaat cactgagtgg tagcgagtct
 1560
 gttggtgtaa ttgcattttt aatgacgcag ccgcagacag cacaaatcca aacggccgtt
 1620
 aaagcaggcc tcaactggtt caatagcccg agcacctatt tggaaggta cacctacgat
 1680
 tcatccaaag cgtccactaa tcccatagtg cagaaagcgg gaagtagaat gtggtatcgc
 1740
 ttttacgatt taaataccaa ccgtggtttt ttcagcgacc gggacggcag caaattctat
 1800
 gacattacca aaatgtctga agaacgtcgc acgggttata gttggggtgg cgcttatggt
 1860
 gagagcatca tcgcctttgg caaaaaagtg ggctatctat aa
 1902

<210> 44
 <211> 633
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> BINDING
 <222> (4)...(89)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (152)...(275)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (277)...(633)
 <223> Catalytic domain

<400> 44

Met	Asp	Pro	Lys	Asn	Trp	Gly	Ser	Gly	Phe	Thr	Gly	Glu	Ile	Lys	Val
1				5					10					15	
Thr	Asn	Asn	Thr	Ser	Gln	Thr	Val	Asn	Ser	Trp	Ser	Val	Ser	Trp	Gln
			20					25					30		
Glu	Ala	Gly	Ala	Ser	Val	Thr	Asn	Ser	Trp	Asn	Ala	Thr	Leu	Gly	Gly
		35					40					45			
Thr	Asn	Pro	Tyr	Thr	Ala	Thr	Gly	Leu	Gly	Trp	Asn	Ser	Thr	Leu	Ala
	50					55					60				
Pro	Gly	Ala	Ser	Ala	Ser	Phe	Gly	Phe	Gln	Ala	Asn	Gly	Thr	Ala	Gly
65					70					75					80
Ala	Pro	Lys	Val	Asn	Gly	Ser	Leu	Cys	Gly	Ala	Thr	Ala	Ser	Ser	Ala
				85					90					95	
Ala	Thr	Ser	Lys	Ser	Ser	Ala	Ser	Val	Ala	Ser	Ser	Lys	Ile	Ala	Ser
			100					105					110		
Ser	Ile	Gln	Ser	Ser	Ala	Thr	Ser	Ser	Ser	Lys	Ser	Ser	Ser	Ser	Ala
		115					120					125			
Ala	Pro	Ser	Ser	Thr	Pro	Lys	Ser	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ala
	130					135						140			
Ser	Phe	Thr	Ile	Gln	Glu	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly
145					150					155					160
Ile	Ala	Thr	Glu	Ser	Thr	Asn	Thr	Gly	Phe	Thr	Gly	Asn	Gly	Tyr	Thr
				165					170					175	
Asn	Ser	Asn	Asn	Val	Gln	Gly	Ala	Ala	Ile	Val	Trp	Ala	Val	Asn	Ala
			180					185					190		
Thr	Thr	Ser	Ala	Arg	His	Thr	Ile	Thr	Phe	Arg	Phe	Ala	Asn	Gly	Gly
		195					200					205			
Thr	Ala	Asn	Arg	Asn	Gly	Ser	Leu	Val	Ile	Asn	Gly	Gly	Ser	Asn	Gly
	210					215					220				
Asn	Tyr	Thr	Val	Gln	Leu	Pro	Arg	Thr	Ala	Ser	Trp	Ala	Asp	Trp	Gln
225					230					235					240
Thr	Val	Ser	Leu	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Asn	Leu	Gln
				245					250					255	
Leu	Thr	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Phe	Ile	Lys
			260					265					270		
Ile	Glu	Gly	Ala	Ser	Thr	Lys	Ala	Gly	Thr	Cys	Ala	Gly	Ala	Val	Ser
		275					280					285			
Ser	Ser	Ser	Val	Ala	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ala	Ala	Ser
	290					295					300				
Ser	Ser	Val	Pro	Thr	Asn	Thr	Gly	Ala	Met	Leu	Thr	Leu	Asp	Gly	Asn
305					310					315					320
Pro	Ala	Ala	Ser	Trp	Leu	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Ser	Ala	Ser
				325					330					335	
Arg	Ala	Asp	Ile	Val	Ala	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro
			340					345					350		
Lys	Asn	Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ala
		355					360					365			
Ser	Gly	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu
	370					375					380				
Ala	Glu	Val	Tyr	Lys	Thr	Gly	Asn	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val
385					390					395					400
Arg	Arg	Ala	Ala	Asn	Phe	Ile	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala
				405					410					415	
Leu	Pro	Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr
			420					425					430		
Phe	Asn	Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala
		435					440					445			
Ala	Asn	Lys	Arg	Ala	Pro	Phe	Asp	Thr	Asp	Val	Phe	Asn	Asp	Thr	Asp
		450				455					460				
Arg	Ala	Lys	Phe	Lys	Thr	Ala	Val	Thr	Lys	Gly	Val	Asp	Tyr	Ile	Leu
465					470					475					480

Lys Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln
 485 490 495
 His Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu
 500 505 510
 Glu Ser Leu Ser Gly Ser Glu Ser Val Gly Val Ile Ala Phe Leu Met
 515 520 525
 Thr Gln Pro Gln Thr Ala Gln Ile Gln Thr Ala Val Lys Ala Gly Leu
 530 535 540
 Asn Trp Phe Asn Ser Pro Ser Thr Tyr Leu Glu Gly Tyr Thr Tyr Asp
 545 550 555 560
 Ser Ser Lys Ala Ser Thr Asn Pro Ile Val Gln Lys Ala Gly Ser Arg
 565 570 575
 Met Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser
 580 585 590
 Asp Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Lys Met Ser Glu Glu
 595 600 605
 Arg Arg Thr Gly Tyr Ser Trp Gly Gly Ala Tyr Gly Glu Ser Ile Ile
 610 615 620
 Ala Phe Gly Lys Lys Val Gly Tyr Leu
 625 630

<210> 45
 <211> 987
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 45
 atgactagac ggccttcat cgcggttattc tgtttcttcg cggccgtctg cgcgcacgcg
 60
 cagtccaccg tgcgctggaa ggacgtgctc gagcagtcgc agggctggta ttccacgacc
 120
 gccgcgcacg tcgtcgccga cacggtgctg ctgtatcaac gtccatccgg tggatggccg
 180
 aaggacatcg acatgacggc gccgccggcg gaccgcactc ctcccgcgcg tccagacgcg
 240
 accatcgaca acggcgccac gaccacgcag atccgcctgc tcgctcgtgc ggcctcgggc
 300
 gcaccggcgg ctgccgccca cacctacacg gcggcgggcg ttcgcgggat cgattacctg
 360
 ctcgagggcg agtatcccaa cggcggtggt ccgcagttct tccccctgcg caaggactat
 420
 tcgcgctacg tcacgttcaa cgacgacgcg atgatgaacg tgatgttcct gctggacgag
 480
 gtctcggcgg gagatgcgcc gttcacgttc gtggacgaac aacgccgcga ccgcgcgcgc
 540
 gctgccgtcg ccaagggggt ctccgtcatc ctgaagtcgc aggtccggat cgacgggacg
 600
 ctgaccgcct ggtgcgcgca acacgacgag atcaccctgg caccgcgtcc ggcgcgcacc
 660
 ttcgagcagc cgctcgtcag cggcaacgag tctgtcgcga tcgtgcgctt cctgatgacc
 720
 cgtccgccga cgccagcgat cgtcgccgcg gtcgatgcgg cggtcgcctg gtcagacgc
 780
 gtccgcctcc ctgacggacg gtgggcccga ttctacgagt tcggtaccaa tcgtccgac
 840
 ttctcggggc gagacagtgt cgtgcgctac aaactcgagg agatcgaaca ggaacgtcag
 900
 gagggctacg cgtggtacgg cacgtggccg aggacgcttg ttgagaagat gtaccctgca

960
tggaagtcgc ggcttccggg caagtag
987

<210> 46
<211> 328
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<221> DOMAIN
<222> (21)...(328)
<223> Catalytic domain

<400> 46
Met Thr Arg Arg Ala Phe Ile Ala Val Ile Cys Phe Phe Ala Ala Val
1 5 10 15
Cys Ala His Ala Gln Ser Thr Val Arg Trp Lys Asp Val Leu Glu Gln
20 25 30
Ser Glu Gly Trp Tyr Ser Thr Thr Ala Ala His Val Val Ala Asp Thr
35 40 45
Val Leu Leu Tyr Gln Arg Pro Ser Gly Gly Trp Pro Lys Asp Ile Asp
50 55 60
Met Thr Ala Pro Pro Ala Asp Arg Thr Pro Pro Ala Arg Pro Asp Ala
65 70 75 80
Thr Ile Asp Asn Gly Ala Thr Thr Thr Gln Ile Arg Leu Leu Ala Arg
85 90 95
Ala Ala Ser Gly Ala Pro Ala Ala Ala Ala His Thr Tyr Thr Ala Ala
100 105 110
Ala Leu Arg Gly Ile Asp Tyr Leu Leu Glu Ala Gln Tyr Pro Asn Gly
115 120 125
Gly Trp Pro Gln Phe Phe Pro Leu Arg Lys Asp Tyr Ser Arg Tyr Val
130 135 140
Thr Phe Asn Asp Asp Ala Met Met Asn Val Met Phe Leu Leu Asp Glu
145 150 155 160
Val Ser Ala Gly Asp Ala Pro Phe Thr Phe Val Asp Glu Gln Arg Arg
165 170 175
Asp Arg Ala Arg Ala Ala Val Ala Lys Gly Val Ser Val Ile Leu Lys
180 185 190
Ser Gln Val Arg Ile Asp Gly Thr Leu Thr Ala Trp Cys Ala Gln His
195 200 205
Asp Glu Ile Thr Leu Ala Pro Arg Pro Ala Arg Thr Phe Glu His Ala
210 215 220
Ser Leu Ser Gly Asn Glu Ser Val Ala Ile Val Arg Phe Leu Met Thr
225 230 235 240
Arg Pro Pro Thr Pro Ala Ile Val Ala Ala Val Asp Ala Ala Val Ala
245 250 255
Trp Leu Arg Arg Val Arg Leu Pro Asp Gly Arg Trp Ala Arg Phe Tyr
260 265 270
Glu Phe Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Ser Val Val
275 280 285
Arg Tyr Lys Leu Glu Glu Ile Glu Gln Glu Arg Gln Glu Gly Tyr Ala
290 295 300
Trp Tyr Gly Thr Trp Pro Arg Thr Leu Val Glu Lys Met Tyr Pro Ala
305 310 315 320
Trp Lys Ser Arg Leu Pro Gly Lys

<210> 47
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 47
 atgaaaaatt ttaaaaaatat tgtaggagcg ttacttatat ctgtaacggt ttgtgtgcac
 60
 gggcaggtaa acaaaaaatc ctggcgggct attacacagt ctaacgacga tgcattggtt
 120
 gcatctgatg gagctgcaca gattgcagat aatgtattac tctatcagcg caatgttggc
 180
 ggatggccta aaaatattga aatgcaggaa ccgcttagtg aggccgacaa aaaaaagctg
 240
 atagatctta agtctacggc caaagaaagt actacagata atggggctac gtgtcaggaa
 300
 atggtattcc tctctaagat atataaaca aagcccgaag agaagtataa agaggctttt
 360
 ttaaaaggac ttaattattt gcttgaagca cagtataaaa atggtggatg gccacagttc
 420
 taccctttaa aaaaagggtt ttatacccac attacctata atgacgattc tatggtaaac
 480
 attcttatga tcttaaagaa tattaaggaa gatgccaaact attacagtat tacgccaaagc
 540
 gataaaagttt taaagcaggc atcgacagct tttgacagag gcattgactg cattctaaaa
 600
 acacagtaca agcaaaaggg tgtgcttaca agctgggtgtg cccagcacga tgagggtaca
 660
 ttagaacctg caaatgcaag ggcttttgag ttggcatcac taagtggtaa agaactctgt
 720
 aaaataacgt tgttgcta atgtgttaaaa aatccgtcta aagagggtgt tgctgctgta
 780
 gatgctgctg tggcgtggtt tgaaaaaaca aaaattgaag gcattaaagt agaagaagta
 840
 accggagctg atggcaaaaa ggatagggtg gtagtacaaa gggctgatgc cgaaccattg
 900
 tgggcgcggt ttatggaaact ggataccaac aggccatttt tttgcgacag ggacggtata
 960
 aaaaaatatt cgcttgctga gatagggtcat gaacgccgta acggatatgg ctggtacacc
 1020
 aacgaaccaa aagaagtttt aaagaaatac accaaatgga aaaacagtct taaatag
 1077

<210> 48
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(358)

<223> Catalytic domain

<400> 48

Met Lys Asn Phe Lys Asn Ile Val Gly Ala Leu Leu Ile Ser Val Thr
1 5 10 15
Phe Cys Val His Gly Gln Val Asn Lys Ser Trp Arg Ala Ile Thr
20 25 30
Gln Ser Asn Asp Asp Ala Trp Phe Ala Ser Asp Gly Ala Ala Gln Ile
35 40 45
Ala Asp Asn Val Leu Leu Tyr Gln Arg Asn Val Gly Gly Trp Pro Lys
50 55 60
Asn Ile Glu Met Gln Glu Pro Leu Ser Glu Ala Asp Lys Lys Lys Leu
65 70 75 80
Ile Asp Leu Lys Ser Thr Ala Lys Glu Ser Thr Thr Asp Asn Gly Ala
85 90 95
Thr Cys Gln Glu Met Val Phe Leu Ser Lys Ile Tyr Lys Gln Lys Pro
100 105 110
Glu Glu Lys Tyr Lys Glu Ala Phe Leu Lys Gly Leu Asn Tyr Leu Leu
115 120 125
Glu Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Lys
130 135 140
Lys Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Ser Met Val Asn
145 150 155 160
Ile Leu Met Ile Leu Lys Asn Ile Lys Glu Asp Ala Asn Tyr Tyr Ser
165 170 175
Ile Thr Pro Ser Asp Lys Val Leu Lys Gln Val Ser Thr Ala Phe Asp
180 185 190
Arg Gly Ile Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Lys Gly Val
195 200 205
Leu Thr Ser Trp Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Ala
210 215 220
Asn Ala Arg Ala Phe Glu Leu Ala Ser Leu Ser Gly Lys Glu Ser Ala
225 230 235 240
Lys Ile Thr Leu Leu Leu Met Ser Val Lys Asn Pro Ser Lys Glu Val
245 250 255
Val Ala Ala Val Asp Ala Ala Val Ala Trp Phe Glu Lys Thr Lys Ile
260 265 270
Glu Gly Ile Lys Val Glu Glu Val Thr Gly Ala Asp Gly Lys Lys Asp
275 280 285
Arg Val Val Val Gln Arg Ala Asp Ala Glu Pro Leu Trp Ala Arg Phe
290 295 300
Met Glu Leu Asp Thr Asn Arg Pro Phe Phe Cys Asp Arg Asp Gly Ile
305 310 315 320
Lys Lys Tyr Ser Leu Ala Glu Ile Gly His Glu Arg Arg Asn Gly Tyr
325 330 335
Gly Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Thr Lys
340 345 350
Trp Lys Asn Ser Leu Lys
355

<210> 49

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 49

atgttaagtt tcatcgcggt atcagtgttt cataattact gcacagggca gacagcgccc
60

accaaaaaatt cagtggccga aaagatgctt cagtaccagt tgtcaaatgg cgcctggccc
 120
 aaacagtttg tagacaaaag tgtcgttgat tacagtcttc cattaacgaa agagcgccta
 180
 cagcagatca agaaaacaga tattgatcat gctacgctcg acaacagtgc gacaaccg
 240
 gaaataactg aattgatcaa ggcttttaag gacactaaaa ataaggcata tttgactgct
 300
 gtagaaaagg ggattgcata tattttatcg gctcaatatg agaatggcgg atttccacaa
 360
 tactacccaa ataaattata ctatagagct gagataacat acaacgatga tgcgatgatc
 420
 aatgcattac tagtgcttta caaagtagcc aataagcgag aggggtttga ggctatcaat
 480
 cccatatttg tgtcaaaagc gcaaaaagca gttgaaaagg gtataacctg tatcctaaaa
 540
 acacaggtca tacaagacgg aaaaaggagt atttgggctg cgcaatacga tcagaacact
 600
 ttacaacctg ctcaggcaag aaagtttgaa ccagcttcat tgagcacaag tgaatctgtt
 660
 tccatcgctt gctttctcat gctacagcct gcaaccactg aaattaagca agcgatcgaa
 720
 catgcaatac aatggttcga acagcatgat attgaagggt accgtttcga ccgcatacaa
 780
 gatagggtga ctggaaaata tcaacggcaa cttgtcgcag atcggacttc cacgatttgg
 840
 gcgcgatttt ataatctcga agacaaccgc ccattgtttg gagatcggga caataacaat
 900
 aaatacaact ttgaggaggt ttcagaggag cgtagaaatg gctatgcttg gttcggcaac
 960
 tggccggaaa agctgatcca aaaggactat ccaaaatgga aaaaacaata caaaattaa
 1020
 taa
 1023

<210> 50
 <211> 340
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(16)

<221> DOMAIN
 <222> (17)...(340)
 <223> Catalytic domain

<400> 50
 Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
 1 5 10 15
 Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
 20 25 30
 Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
 35 40 45
 Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Arg Leu Gln Gln Ile Lys
 50 55 60
 Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
 65 70 75 80

540
 acgggctggt gccagcagca tgacgagcgc tccctcgccc ccaccaaggc tcgcgccctac
 600
 gagcaccat cgatcgccag caaggaaacg gtaaccatca cgcgcttcct catgaccctc
 660
 gatcgcccga gtcagcagat catcgcggcg atcgaggcgg ctgtcgagt gttgcgcgtg
 720
 gcgaccctgt cgggtgtgcg agttgagcgt cggccggacc cggcgagtcc gaccggatat
 780
 gacgtcgctg ccgcgccgga tgccgccgca cctccgacct gggcacggtt ctacgagatc
 840
 ggcacgaacc gcccaatgtt ttccggccgc gacggcgtga tcagattccg gctcgcgga
 900
 atcgagattg agcgccgcac cggctacagc tggatgggcg actatgccgc gaggttgctg
 960
 aacgaggagt atccggcgtg ggcgaggcta cgccgggcga gctttcagaa cgccgagctg
 1020
 cacaaggagt ccggtgaagt cgtacacacg gcgatcgtgc acgatcttgc cttccttgat
 1080
 gtcgaagaca aagaccagcc gcagccgaaa gtgcttttcg ctgggcggta g
 1131

<210> 52
 <211> 376
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(376)
 <223> Catalytic domain

<400> 52
 Met Thr Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp Tyr Gly Gly
 1 5 10 15
 Pro Glu Ala Arg Arg Ile Ala Asn Leu Val Leu Leu Tyr Gln Arg Ala
 20 25 30
 Thr Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Arg Ser Leu Ser Pro
 35 40 45
 Asp Asp Arg Thr Thr Leu Ala Ala Glu Arg Ala Leu Thr Asp Ser Thr
 50 55 60
 Ile Asp Asn Gly Ser Thr Thr Thr Gln Leu Arg Phe Leu Ala Met Val
 65 70 75 80
 Gln His Ala Gln Gln Ala Pro Val Arg Asp Ala Ile Thr His Gly Leu
 85 90 95
 Asp Tyr Leu Leu Asn Ala Gln Tyr Ser Asn Gly Gly Trp Pro Gln Tyr
 100 105 110
 Phe Pro Leu Arg Asp Asp Tyr Ser Arg His Ile Thr Phe Asn Asp Asp
 115 120 125
 Ala Met Ile Asn Val Met Thr Val Leu Arg Asp Val Ala Glu Ala Arg
 130 135 140
 Met Pro Phe Glu Gly Ile Asp Ala Val Arg Arg Asp Arg Ala Arg Val
 145 150 155 160
 Ala Ile Thr Arg Gly Ile Asp Val Ile Leu Gly Thr Gln Ile Arg Val
 165 170 175
 Gly Asp Arg Leu Thr Gly Trp Cys Gln His Asp Glu Arg Ser Leu
 180 185 190
 Ala Pro Thr Lys Ala Arg Ala Tyr Glu His Pro Ser Ile Ala Ser Lys
 195 200 205

Glu	Thr	Val	Thr	Ile	Thr	Arg	Phe	Leu	Met	Thr	Leu	Asp	Arg	Pro	Ser
210						215					220				
Gln	Gln	Ile	Ile	Ala	Ala	Ile	Glu	Ala	Ala	Val	Glu	Trp	Leu	Arg	Val
225				230						235					240
Ala	Thr	Leu	Ser	Gly	Val	Arg	Val	Glu	Arg	Arg	Pro	Asp	Pro	Ala	Ser
				245					250					255	
Pro	Thr	Gly	Tyr	Asp	Val	Val	Ala	Ala	Pro	Asp	Ala	Ala	Ala	Pro	Pro
			260					265					270		
Thr	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Met	Phe	Ser
		275					280				285				
Gly	Arg	Asp	Gly	Val	Ile	Arg	Phe	Arg	Leu	Ala	Asp	Ile	Glu	Ile	Glu
	290					295					300				
Arg	Arg	Thr	Gly	Tyr	Ser	Trp	Met	Gly	Asp	Tyr	Ala	Ala	Arg	Leu	Leu
305					310					315					320
Asn	Glu	Glu	Tyr	Pro	Ala	Trp	Ala	Arg	Leu	Arg	Arg	Ala	Ser	Phe	Gln
				325					330					335	
Asn	Ala	Glu	Leu	His	Lys	Glu	Ser	Gly	Glu	Val	Val	His	Thr	Ala	Ile
			340					345					350		
Val	His	Asp	Leu	Ala	Phe	Leu	Asp	Val	Glu	Asp	Lys	Asp	Gln	Pro	Gln
		355					360					365			
Pro	Lys	Val	Leu	Phe	Ala	Gly	Arg								
	370					375									

<210> 53
 <211> 1977
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 53
 atgaataact caacaaaaaa aatgattcgg ccaactcaagg catcttttgc cttgggcgct
 60
 ctcgcactgg caatcgcata accctcatgg gcggcttgct cttacagcgt aaccaataat
 120
 tggggctctg gctttaccgg agaaattaaa gtaaccaacg atacaacatc gactgtaaat
 180
 aattgggtctg tgtcttggca ggaatcaggc gtgaccgtca ctaacgcata gaatgcaaca
 240
 ctgagcggat caaatcctta taccgcaaca tcaactcggg ggaacggaac tctcgtccca
 300
 aaagcttcag caagttttgg ttttcaagca aatggaacag cgggcgcacc gaaagtaaat
 360
 ggaaccttgt gtggtaccag cacatcatca acagggtacat cctcagttgc acctcatcc
 420
 gtagcgagta gcgttgctgt atcaagcagt aaatcatcaa gctctgttgc aaccatcagt
 480
 agctctaaat ccagcagcag tgtgccgaca gtttcatcat tcactattca ggaagagcaa
 540
 gccggtttct gccgtgtaga tggcattgca actgaaagta ctaacactgg ctatacaggt
 600
 aatggctaca ccaacaccac taatgcgcaa ggcgctgcaa ttgaatgggc aattaatgct
 660
 cccaacagca gccgtacac cctcaccttc cgttatgcca atgctggtac cgctaatacgc
 720
 aatgggttcgt tattaattaa cgacggaagc aatggtaact acacagtga attgccaagt
 780
 accggcgcat gggcaacctg gcaaaccgtc agtggtgaag tggatttggt gcaaggcaat
 840
 aatattttga aactcgcttc gcttactgct gatggccttg cgaatataga ttcattaaaa

900
 attgaaggcg cacaagccaa agctgggtgta tgcagcacta cggttaagtag cagctcttcg
 960
 tcaattaaat caagttccag ttcattcatcg tccagctcaa ctgcagcagt aaaaacatta
 1020
 aactggatg gtaaccctgc tgcaaaactgg tttaataaat ccagaaccaa gtggaatgtc
 1080
 agcagagctg acatcgctact ttcgtatcag caatcaaagt gtggctggcc aaaaaatttg
 1140
 gactacaact cggtaggctc aggtaatggg ggtagcgaca gcggcactat tgataatggg
 1200
 gcaaccataa ccgaaatggg gtacctcgct gaagtgtata aaaatggcgg gaataccaaa
 1260
 taccgcgacg ccgtgcgcag agcagcgaat tttattgtga gttcacaata cagcactggg
 1320
 gctttaccgc agttttatcc gctgaaagggt gggtacgcag atcacgctac ctttaatgat
 1380
 aatgggtatg cttacgcgtt gactgttctg gatttcgcgg taaataaacg cgcgccattt
 1440
 gataacgata ttttctctga ctctgaccgc agcaaattta aaactgctgt taccaaaggc
 1500
 gtcgattaca tattaanaagc gcaatggaaa cagaatggaa aattaaccgt atgggtgcgca
 1560
 caacacggtg ctaatgatta tcaaccgaaa aaagcgcgtg cttacgagtt agaattcattg
 1620
 agtggtagtg aatctgtcgg tgtactcgct ttcttaataga ctcaaccaca aaccacgcaa
 1680
 attgaagcag ctgtgcgtgc aggtgtggcc tggtttaata gcccaagcac ctacttgaat
 1740
 aattacactt acgattcttc caaagcttcg accaatccaa tcgtgccaaa atccggaagc
 1800
 aaaatgtggg atcgctttta tgacctgaat accaaccgcg gtttcttcag tgatcgtgac
 1860
 ggcagcaagt tctacgacat caccctaaatg tcagaagagc gtcgcactgg ttacagttgg
 1920
 ggtgggtgact acggcagctc gattatcagc ttcgcacaaa aagtgggata tctctaa
 1977

<210> 54
 <211> 658
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(31)

<221> BINDING
 <222> (32)...(124)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (180)...(303)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (304)...(658)
 <223> Catalytic domain

<400> 54

Met	Asn	Asn	Ser	Thr	Lys	Lys	Met	Ile	Arg	Pro	Leu	Lys	Ala	Ser	Phe
1				5					10					15	
Ala	Leu	Gly	Ala	Leu	Ala	Leu	Ala	Ile	Ala	Ser	Pro	Ser	Trp	Ala	Ala
			20					25					30		
Cys	Ser	Tyr	Ser	Val	Thr	Asn	Asn	Trp	Gly	Ser	Gly	Phe	Thr	Gly	Glu
		35					40					45			
Ile	Lys	Val	Thr	Asn	Asp	Thr	Thr	Ser	Thr	Val	Asn	Asn	Trp	Ser	Val
	50					55					60				
Ser	Trp	Gln	Glu	Ser	Gly	Val	Thr	Val	Thr	Asn	Ala	Trp	Asn	Ala	Thr
65					70					75				80	
Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Ala	Thr	Ser	Leu	Gly	Trp	Asn	Gly
				85					90					95	
Thr	Leu	Ala	Pro	Lys	Ala	Ser	Ala	Ser	Phe	Gly	Phe	Gln	Ala	Asn	Gly
			100						105				110		
Thr	Ala	Gly	Ala	Pro	Lys	Val	Asn	Gly	Thr	Leu	Cys	Gly	Thr	Ser	Thr
		115					120					125			
Ser	Ser	Thr	Gly	Thr	Ser	Ser	Val	Ala	Pro	Ser	Ser	Val	Ala	Ser	Ser
	130					135					140				
Val	Ala	Val	Ser	Ser	Ser	Lys	Ser	Ser	Ser	Ser	Val	Ala	Thr	Ile	Ser
145					150					155				160	
Ser	Ser	Lys	Ser	Ser	Ser	Ser	Val	Pro	Thr	Val	Ser	Ser	Phe	Thr	Ile
				165					170					175	
Gln	Glu	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly	Ile	Ala	Thr	Glu
			180					185					190		
Ser	Thr	Asn	Thr	Gly	Tyr	Thr	Gly	Asn	Gly	Tyr	Thr	Asn	Thr	Thr	Asn
		195					200					205			
Ala	Gln	Gly	Ala	Ala	Ile	Glu	Trp	Ala	Ile	Asn	Ala	Pro	Asn	Ser	Ser
	210					215					220				
Arg	Tyr	Thr	Leu	Thr	Phe	Arg	Tyr	Ala	Asn	Ala	Gly	Thr	Ala	Asn	Arg
225					230					235				240	
Asn	Gly	Ser	Leu	Leu	Ile	Asn	Asp	Gly	Ser	Asn	Gly	Asn	Tyr	Thr	Val
				245					250					255	
Gln	Leu	Pro	Ser	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Thr	Val	Ser	Val
			260					265				270			
Glu	Val	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu	Ala	Ser	Leu
		275					280					285			
Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile	Glu	Gly	Ala
	290					295					300				
Gln	Ala	Lys	Ala	Gly	Val	Cys	Ser	Thr	Thr	Val	Ser	Ser	Ser	Ser	Ser
305					310					315					320
Ser	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ala	Ala
				325					330					335	
Val	Lys	Thr	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala	Ala	Asn	Trp	Phe	Asn
			340					345					350		
Lys	Ser	Arg	Thr	Lys	Trp	Asn	Val	Ser	Arg	Ala	Asp	Ile	Val	Leu	Ser
		355					360					365			
Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn	Leu	Asp	Tyr	Asn	Ser
	370					375					380				
Val	Gly	Ser	Gly	Asn	Gly	Gly	Ser	Asp	Ser	Gly	Thr	Ile	Asp	Asn	Gly
385					390					395				400	
Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala	Glu	Val	Tyr	Lys	Asn	Gly
				405					410					415	
Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg	Arg	Ala	Ala	Asn	Phe	Ile
			420					425					430		
Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu	Pro	Gln	Phe	Tyr	Pro	Leu
		435					440					445			
Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe	Asn	Asp	Asn	Gly	Met	Ala
	450					455					460				
Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val	Asn	Lys	Arg	Ala	Pro	Phe
465					470					475					480

Asp	Asn	Asp	Ile	Phe	Ser	Asp	Ser	Asp	Arg	Ser	Lys	Phe	Lys	Thr	Ala
				485					490					495	
Val	Thr	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys	Ala	Gln	Trp	Lys	Gln	Asn
			500					505					510		
Gly	Lys	Leu	Thr	Val	Trp	Cys	Ala	Gln	His	Gly	Ala	Asn	Asp	Tyr	Gln
		515					520					525			
Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu	Ser	Leu	Ser	Gly	Ser	Glu
	530					535					540				
Ser	Val	Gly	Val	Leu	Ala	Phe	Leu	Met	Thr	Gln	Pro	Gln	Thr	Thr	Gln
545					550					555					560
Ile	Glu	Ala	Ala	Val	Arg	Ala	Gly	Val	Ala	Trp	Phe	Asn	Ser	Pro	Ser
				565					570						575
Thr	Tyr	Leu	Asn	Asn	Tyr	Thr	Tyr	Asp	Ser	Ser	Lys	Ala	Ser	Thr	Asn
			580					585						590	
Pro	Ile	Val	Pro	Lys	Ser	Gly	Ser	Lys	Met	Trp	Tyr	Arg	Phe	Tyr	Asp
		595					600					605			
Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp	Arg	Asp	Gly	Ser	Lys	Phe
	610					615					620				
Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg	Arg	Thr	Gly	Tyr	Ser	Trp
625					630					635					640
Gly	Gly	Asp	Tyr	Gly	Ser	Ser	Ile	Ile	Ser	Phe	Ala	Gln	Lys	Val	Gly
				645					650					655	
Tyr	Leu														

<210> 55
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 55
 gtggtcctag gtaataacgg cggcagcttg agttgcgtcc aatatattgt gattgtgaaa
 60
 ggacccggtg gacctcgacc gccggtgaaa ccggccgtcc aggcgcccgt tagggttacc
 120
 tggagcgcac gcctagtcca gcggcccga tggtagggga gtgacgaagc gatccgcac
 180
 gcggacaacg tcctcctcta ccagcgcaac accggcgggt ggccgaagga catagatatg
 240
 gccgagccca tcccgaaca caggaagtcc tttttcctca ccgagaagga gcggaccgat
 300
 gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgc ccgcgtctac
 360
 aaggcgacca ggctggaacg gttcaaggag ggcttcctca aaggtctcga ctacctcttg
 420
 gccgcccagt acccgaacgg cggctggccc cagtattatc ctaacttgag gggctactac
 480
 gccaacatca cttataacga caatgccatg gtgaacgtgc tcacctcctt ccagagcatc
 540
 gccaaaaagg ccccggagta cgacttcgtc gaccgcggcg gccgggagaa ggccgcccgg
 600
 gccgtggcga aagggatcga ctgcacctc aagaccaga tccgtgtcaa tggaaaactt
 660
 accgcctggt gcgcccagca tgacccaag acgctggcg ccgcgccggc ccgttcgtat
 720
 gagcttgagt ccacagcgg tttcgagagc gtcgggatcg tccggttctt aatgagcctc
 780
 gagaatccga gcccgaaagt catcgaggcg gtagaggccg ccgtgaaatg gttcgaggag

840
gtcaagctta ccgggatcaa ggtggtcgag aaacccgacc cgtcccttcc gggcggttac
900
gaccgcgtgg tggtcgaaga cccaacgcg ccgcccattct gggcccgggtt ctacgagatc
960
ggcaccaacc gtcccttctt ctgcggccgc gatggatatca aaaaatacag cctggcggag
1020
atcgaacacg aacgccgggt cggttactcc tggtagacca atgccccggc ctacctcatc
1080
gagaaggagt atccgctctg gcgggcaaaa caccctacca agtaa
1125

<210> 56
<211> 374
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(374)
<223> Catalytic domain

<400> 56
Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
1 5 10 15
Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
20 25 30
Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Cys Leu Val Gln Arg
35 40 45
Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
50 55 60
Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
65 70 75 80
Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys
85 90 95
Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
100 105 110
Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
115 120 125
Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
130 135 140
Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
145 150 155 160
Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
165 170 175
Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
180 185 190
Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
195 200 205
Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
210 215 220
Ala Gln His Asp Pro Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
225 230 235 240
Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
245 250 255
Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
260 265 270
Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
275 280 285

Val	Glu	Lys	Pro	Asp	Pro	Ser	Leu	Pro	Gly	Gly	Tyr	Asp	Arg	Val	Val
	290					295					300				
Val	Glu	Asp	Pro	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile
305					310					315					320
Gly	Thr	Asn	Arg	Pro	Phe	Phe	Cys	Gly	Arg	Asp	Gly	Ile	Lys	Lys	Tyr
				325					330					335	
Ser	Leu	Ala	Glu	Ile	Glu	His	Glu	Arg	Arg	Val	Gly	Tyr	Ser	Trp	Tyr
			340					345					350		
Thr	Asn	Ala	Pro	Ala	Tyr	Leu	Ile	Glu	Lys	Glu	Tyr	Pro	Leu	Trp	Arg
		355					360					365			
Ala	Lys	His	Pro	Thr	Lys										
	370														

<210> 57
 <211> 1170
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 57
 atggacaaac gcg tcaaatg gattcatcag ctttcaaaag aagaagcaaa gcagttcgag
 60
 cccgaaaatt tcctcaaagg caaagacggc tggaatccga aaaaggcgga tgaccgctgg
 120
 ctcgaaaaaa caaacctga ctggcagctc gttacgtgga acgacgcgtt acgccaggcg
 180
 ccgtcttggg atcaaaccga tgaagcggcg cgcattgccg accaggtgat tttgtaccag
 240
 aaagacaacg gcggctggga aaaaaatctc gatatgacgg cgatgctcac gcaagccgaa
 300
 cgcgaaaagc tcgccaaaga aaaatcgaac acgtcggaaa cgacgatcga caaccgcacg
 360
 acctacacgc aagtcgcttt tctcgccaaa gtcattacgg gcagcttgca gaaaacgact
 420
 ccgccgacca atttcccga acataaggaa gcttttttca agggcttgga ttacctgctc
 480
 gcgtcgcagt acgaatcggg cggctttccg cagttttatc cgctcaaaaa aggttattac
 540
 acgcacatca cgttcaacga cgatgcgatg attggcggtt tgaagggttt gcgcgaaatc
 600
 gccaaaaaga aggaagacta tctttttgtt gacgaagaac gccgcctgaa agcggaaaaa
 660
 tcggtcgaag aagcgtgcc gctgattctg aaattgcagg ttgaagtcgg cggcaaaaaa
 720
 acggtttggg cggcgcagta tgacgaaaac acttttaaac ccgcagcggc gcgaaagttt
 780
 gaaccgggtt cttaacggc gggcgaatcg gtcggcatcg tccgggtttt aatgtacgat
 840
 tcaaagccc accaggcgac gattgacgcg attgaatctg ccattcagtg gtatcgcgcg
 900
 aacaaaatcg aaggcattcg atgggtgcgc gaaaacggcg aaaaccgcgt cgtcaaggac
 960
 aaaaacgcgc cgccgatttg ggcgcggttt tacgaaatcg aaacgatgaa gccgattttc
 1020
 atcggggcgc acgcatcat tcgttacgac gtgtctgaaa tcgaagccga gcgccgcaac
 1080
 ggctacgcgt ggtacgtctc ggagccgaac gagctgcttg aaaaagatta cccgaaatgg
 1140
 ctggaaaaaa ttaaaaaatc agtaaagtaa

1170

<210> 58
<211> 389
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(389)
<223> Catalytic domain

<400> 58

Met	Asp	Lys	Arg	Val	Lys	Trp	Ile	His	Gln	Leu	Ser	Lys	Glu	Glu	Ala	
1				5					10					15		
Lys	Gln	Phe	Glu	Pro	Glu	Asn	Phe	Leu	Lys	Gly	Lys	Asp	Gly	Trp	Asn	
			20					25					30			
Pro	Lys	Lys	Ala	Asp	Asp	Arg	Trp	Leu	Glu	Lys	Thr	Lys	Pro	Asp	Trp	
		35					40					45				
Gln	Leu	Val	Thr	Trp	Asn	Asp	Ala	Leu	Arg	Gln	Ala	Pro	Leu	Trp	Tyr	
	50					55					60					
Gln	Thr	Asp	Glu	Ala	Ala	Arg	Ile	Ala	Asp	Gln	Val	Ile	Leu	Tyr	Gln	
65					70				75						80	
Lys	Asp	Asn	Gly	Gly	Trp	Glu	Lys	Asn	Leu	Asp	Met	Thr	Ala	Met	Leu	
			85						90					95		
Thr	Gln	Ala	Glu	Arg	Glu	Lys	Leu	Ala	Lys	Glu	Lys	Ser	Asn	Thr	Ser	
			100					105					110			
Glu	Thr	Thr	Ile	Asp	Asn	Arg	Thr	Thr	Tyr	Thr	Gln	Val	Ala	Phe	Leu	
	115						120					125				
Ala	Lys	Val	Ile	Thr	Gly	Ser	Leu	Gln	Lys	Thr	Thr	Pro	Pro	Thr	Asn	
	130					135					140					
Phe	Pro	Lys	His	Lys	Glu	Ala	Phe	Phe	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	
145					150				155						160	
Ala	Ser	Gln	Tyr	Glu	Ser	Gly	Gly	Phe	Pro	Gln	Phe	Tyr	Pro	Leu	Lys	
				165					170					175		
Lys	Gly	Tyr	Tyr	Thr	His	Ile	Thr	Phe	Asn	Asp	Asp	Ala	Met	Ile	Gly	
		180						185					190			
Val	Leu	Lys	Val	Leu	Arg	Glu	Ile	Ala	Lys	Lys	Lys	Glu	Asp	Tyr	Leu	
	195						200					205				
Phe	Val	Asp	Glu	Glu	Arg	Arg	Leu	Lys	Ala	Glu	Lys	Ser	Val	Glu	Lys	
	210					215						220				
Ala	Leu	Pro	Leu	Ile	Leu	Lys	Leu	Gln	Val	Glu	Val	Gly	Gly	Lys	Lys	
225					230					235					240	
Thr	Val	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Asn	Thr	Phe	Lys	Pro	Ala	Ala	
			245						250					255		
Ala	Arg	Lys	Phe	Glu	Pro	Val	Ser	Leu	Thr	Ala	Gly	Glu	Ser	Val	Gly	
		260						265					270			
Ile	Val	Arg	Phe	Leu	Met	Tyr	Asp	Ser	Lys	Pro	Asp	Gln	Ala	Thr	Ile	
	275						280					285				
Asp	Ala	Ile	Glu	Ser	Ala	Ile	Gln	Trp	Tyr	Arg	Ala	Asn	Lys	Ile	Glu	
	290					295					300					
Gly	Ile	Arg	Trp	Val	Arg	Glu	Asn	Gly	Glu	Asn	Arg	Val	Val	Lys	Asp	
305					310					315					320	
Lys	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Glu	Thr	Met	
			325						330					335		
Lys	Pro	Ile	Phe	Ile	Gly	Arg	Asp	Ala	Ile	Ile	Arg	Tyr	Asp	Val	Ser	
		340						345					350			
Glu	Ile	Glu	Ala	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Tyr	Val	Ser	Glu	
		355					360						365			

Pro Asn Glu Leu Leu Glu Lys Asp Tyr Pro Lys Trp Leu Glu Lys Ile
 370 375 380
 Lys Lys Ser Val Lys
 385

<210> 59
 <211> 1080
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 59
 atgagaatcc ggtcctcttc aatcgcggtc ggcctgattt gcagtctggc gctaagggtg
 60
 cctgcgcaag cgcaggtcac cgtgcgctgg gcgagctcc tgaaccagcc cgccgctgg
 120
 tatggcaccg atgaagcccg tcgaattgcc gaccacgtgc tcgagcatca acgagcggaa
 180
 ggcggtggc caaagaacac ggacatgacc gcagcgcccg atccggcggg gctcacagcc
 240
 gcgcgagtga agccagactc gacgatcgat aacggcgcgga ccgtcactga aatgcgcgtc
 300
 ctgcgcgcgc tctaccgttc atcacccgat ccccgttatc gcgatgcgct gctcaagggt
 360
 ctgcactatc tggtggcagc gcagtatgcc aacggcgggc ggccgcagtt ctaccgcctc
 420
 cggcaggact attcgcgcta tatcacgttc aacgacaacg cgatgatcaa tgcgtgacg
 480
 ctgctctcag acgtcgctgc cggaaatggc gactgggctg ttgctgatgc cagccggcgc
 540
 gagaaaagcc ggacggctgt agagaaggcc gtagaagtca tcctgcgcgc gcaggtgaga
 600
 gttgacggcc ggctgaccgc gtggtgcgcc caacacgacg aggtgacact cgagccgcgc
 660
 aaggcccgcg cctacgaaca tccgtcgctg agcggacagg agacggtggg gatcatccgg
 720
 tttctcatga cccgcgataa accggatcag agagtcgtcg atgcaatcga ggcgtcagtg
 780
 gcatggctga aggcggtgca gctcaaagga cttcgcgtcg accagcgccg cgatccctcg
 840
 ctgccggagg ggcgtgacgt ggtgaccgtc gctgaccctg cggcgccgcc gctctggggc
 900
 cgcttctacg aaatcgggac caatcgcccg atcttctctg gacgcgacgg cgtgatccga
 960
 tactcgctgg cagagatcga gcacgaacgc cggatagggt acgcctggct cggaacctgg
 1020
 cccgcgaagc tgctcgatac cgaataccca tcctggcgac ggactcaaca aaggccgtga
 1080

<210> 60
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(24)

<221> DOMAIN
 <222> (25)...(359)
 <223> Catalytic domain

<400> 60

Met	Arg	Ile	Arg	Ser	Ser	Ser	Ile	Ala	Phe	Gly	Leu	Ile	Cys	Ser	Leu
1				5					10					15	
Ala	Leu	Arg	Val	Pro	Ala	Gln	Ala	Gln	Val	Thr	Val	Arg	Trp	Ala	Asp
			20					25					30		
Val	Leu	Asn	Gln	Pro	Ala	Ala	Trp	Tyr	Gly	Thr	Asp	Glu	Ala	Arg	Arg
		35					40					45			
Ile	Ala	Asp	His	Val	Leu	Glu	His	Gln	Arg	Ala	Glu	Gly	Gly	Trp	Pro
	50					55					60				
Lys	Asn	Thr	Asp	Met	Thr	Ala	Ala	Pro	Asp	Pro	Ala	Val	Leu	Thr	Ala
65					70					75					80
Ala	Arg	Val	Lys	Pro	Asp	Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Val	Thr
				85					90					95	
Glu	Met	Arg	Val	Leu	Ala	Arg	Val	Tyr	Arg	Ser	Ser	Pro	Asp	Pro	Arg
			100					105					110		
Tyr	Arg	Asp	Ala	Leu	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ala	Gln
		115					120					125			
Tyr	Ala	Asn	Gly	Gly	Trp	Pro	Gln	Phe	Tyr	Pro	Leu	Arg	Gln	Asp	Tyr
	130					135					140				
Ser	Arg	Tyr	Ile	Thr	Phe	Asn	Asp	Asn	Ala	Met	Ile	Asn	Val	Val	Thr
145					150					155					160
Leu	Leu	Ser	Asp	Val	Ala	Ala	Gly	Asn	Gly	Asp	Trp	Ala	Phe	Ala	Asp
				165					170					175	
Ala	Ser	Arg	Arg	Glu	Lys	Ser	Arg	Thr	Ala	Val	Glu	Lys	Ala	Val	Glu
			180					185					190		
Val	Ile	Leu	Arg	Ala	Gln	Val	Arg	Val	Asp	Gly	Arg	Leu	Thr	Ala	Trp
		195					200					205			
Cys	Ala	Gln	His	Asp	Glu	Val	Thr	Leu	Glu	Pro	Arg	Lys	Ala	Arg	Ala
	210					215					220				
Tyr	Glu	His	Pro	Ser	Leu	Ser	Gly	Gln	Glu	Thr	Val	Gly	Ile	Ile	Arg
225					230					235					240
Phe	Leu	Met	Thr	Arg	Asp	Lys	Pro	Asp	Gln	Arg	Val	Val	Asp	Ala	Ile
				245					250					255	
Glu	Ala	Ser	Val	Ala	Trp	Leu	Lys	Ala	Val	Gln	Leu	Lys	Gly	Leu	Arg
			260					265					270		
Val	Asp	Gln	Arg	Arg	Asp	Pro	Ser	Leu	Pro	Glu	Gly	Arg	Asp	Val	Val
		275					280					285			
Thr	Val	Ala	Asp	Pro	Ser	Ala	Pro	Pro	Leu	Trp	Ala	Arg	Phe	Tyr	Glu
	290					295					300				
Ile	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Ser	Gly	Arg	Asp	Gly	Val	Ile	Arg
305					310					315					320
Tyr	Ser	Leu	Ala	Glu	Ile	Glu	His	Glu	Arg	Arg	Ile	Gly	Tyr	Ala	Trp
				325					330					335	
Leu	Gly	Thr	Trp	Pro	Ala	Lys	Leu	Leu	Asp	Thr	Glu	Tyr	Pro	Ser	Trp
		340						345					350		
Arg	Arg	Thr	Gln	Gln	Arg	Pro									
				355											

<210> 61
 <211> 1224
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 61
 gtggaattac cagtaaccgg cgcatgggca acctggcaaa ccgcaactgt tgaaattgat
 60
 ttggtgcaag gtaacaacct gttaaaactt tctgcatca cggctgatgg tttggcaa
 120
 atcgattcgt tgaaaattga cggcgacaaa accaaagccg gcgtgtgcag cactgtggca
 180
 agcagcagct cttcatccgt tgcttcatcg attaaatcaa gctccagttc atcctcttcc
 240
 agttcaacga cgacggtaaa aacattaaca ctggatggca accccgcagc aaactgggtt
 300
 aacaaatcca gaaccaaag gaataccagc agagccgatg ttgtactttc ctatcaacaa
 360
 tccaacggcg gctggccaaa aaatctcgat tacaattcag taagcgcagg taatggcggc
 420
 agcgatagcg gcaccatcga taacggtgca accattactg aaatgggtta tctcgcggaa
 480
 gtttacaaaa atggcaacaa caccaagtat cgcatgaggc tgccgagagc cgcaaatttt
 540
 attgtcagct cgcaatacag cactggtgca ttaccacaat tttatccatt gaaaggcggc
 600
 tatgcagacc acgccacctt taacgataac ggcatggcat atgcattaac ggtattggat
 660
 tttgcagtca acaaacgcgc cccatttgat actgatgttt tctccgattc tgatcgcgcg
 720
 aaattcaaaa ccgctgttgc caaagggtgt gattacattt tgaaagcgca gtggaaacaa
 780
 aacggaaaaat taaccgtgtg gtgtgcacaa catggtgcta ccgattatca accgaaaaaa
 840
 gcgcgcgcct atgaattgga atcactgagt ggcagcgaat ctgttggtgt actcgtttc
 900
 ttgatgaccc aaccgcaaac cgcacaaatt gaagccgctg taaaagccgg tgtagcctgg
 960
 ttcaatagcc ccaacacgta tttgaacaat tacacttacg actcttcaaa agcgtcaact
 1020
 aatccaatag ttgccaagtc tggaagcaaa atgtggtatc gcttttacga tttaaatacc
 1080
 aatcgtggct tcttcagtga tcgcatggc agcaaatctt atgacatcac ccagatgtca
 1140
 gaagagcgtc gcactggata tagctggggt ggtgattacg gcacgtcgat tatttccttc
 1200
 gcgcaaaaag tgggatattc gtaa
 1224

<210> 62
 <211> 407
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (0)...(407)
 <223> Catalytic domain

<400> 62
 Met Glu Leu Pro Val Thr Gly Ala Trp Ala Thr Trp Gln Thr Ala Thr
 1 5 10 15
 Val Glu Ile Asp Leu Val Gln Gly Asn Asn Leu Leu Lys Leu Ser Ala
 20 25 30

Ile	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile	Asp	Gly
		35					40					45			
Ala	Gln	Thr	Lys	Ala	Gly	Val	Cys	Ser	Thr	Val	Ala	Ser	Ser	Ser	Ser
		50				55					60				
Ser	Ser	Val	Ala	Ser	Ser	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
65					70					75					80
Ser	Ser	Thr	Thr	Thr	Val	Lys	Thr	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala
				85					90					95	
Ala	Asn	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Thr	Ser	Arg	Ala
			100					105					110		
Asp	Val	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn
		115					120					125			
Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser	Gly
	130					135					140				
Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala	Glu
145					150					155					160
Val	Tyr	Lys	Asn	Gly	Asn	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg	Arg
			165						170					175	
Ala	Ala	Asn	Phe	Ile	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu	Pro
			180					185					190		
Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe	Asn
		195					200					205			
Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val	Asn
	210					215					220				
Lys	Arg	Ala	Pro	Phe	Asp	Thr	Asp	Val	Phe	Ser	Asp	Ser	Asp	Arg	Ala
225					230					235					240
Lys	Phe	Lys	Thr	Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys	Ala
			245						250					255	
Gln	Trp	Lys	Gln	Asn	Gly	Lys	Leu	Thr	Val	Trp	Cys	Ala	Gln	His	Gly
			260					265					270		
Ala	Thr	Asp	Tyr	Gln	Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu	Ser
		275					280					285			
Leu	Ser	Gly	Ser	Glu	Ser	Val	Gly	Val	Leu	Ala	Phe	Leu	Met	Thr	Gln
	290					295					300				
Pro	Gln	Thr	Ala	Gln	Ile	Glu	Ala	Ala	Val	Lys	Ala	Gly	Val	Ala	Trp
305					310					315					320
Phe	Asn	Ser	Pro	Asn	Thr	Tyr	Leu	Asn	Asn	Tyr	Thr	Tyr	Asp	Ser	Ser
			325						330					335	
Lys	Ala	Ser	Thr	Asn	Pro	Ile	Val	Ala	Lys	Ser	Gly	Ser	Lys	Met	Trp
			340					345					350		
Tyr	Arg	Phe	Tyr	Asp	Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp	Arg
		355					360					365			
Asp	Gly	Ser	Lys	Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg	Arg
	370					375					380				
Thr	Gly	Tyr	Ser	Trp	Gly	Gly	Asp	Tyr	Gly	Thr	Ser	Ile	Ile	Ser	Phe
385					390					395					400
Ala	Gln	Lys	Val	Gly	Tyr	Leu									
				405											

<210> 63
 <211> 1023
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 63
 atgttaagtt tcatcgcggt atcagtgttt cataattact gtacagggca gactgcgtcc
 60
 accaaaaatt cagtggccga aaagatgctt cagtaccagt tgtcaaatgg cgcctggccc

120
 aaacagttgg tagacaaaag tgtcgttgat tacagtcttc cattaacgaa agagctccta
 180
 cagcagatca agaaaacaga tattgatcat gctacgctcg acaacagtgc gacaaccgg
 240
 gaaataactg aattgatcaa ggcttttaag gacactaaaa ataaggcata tttgactgct
 300
 gcagaaaagg ggattgcata tatttttatcg gctcaatatg agaatggcgg atttccacaa
 360
 tactacccaa ataaattata ctatagagct gagataacat acaacgatga tgcgatgatc
 420
 aatgcattac tagtgcttta caaagtagcc aataagcgag aggggtttga ggctatcaat
 480
 cccatatttg tgtcaaaagc gcaaaaagca gttgaaaagg gtataacctg tatictaaaa
 540
 acacaggtca tacaagacgg aaaaaggagt atttgggctg cgcaatacga tcagaacact
 600
 ttacaacctg ctcaggcaag aaagtgtgaa ccagcttcat tgagcacaag tgaatctgtt
 660
 tccatcgttc gctttctcat gctacagcct gcaaccactg aaattaagca agcgatcgaa
 720
 catgcaatac aatgggtcga acagcatgat attgaagggt accgtttcga ccgcatacaa
 780
 gataggtgga ctggaaaata tcaacggcag cttgtcgctg atcggacttc cacgatttgg
 840
 gcgcgatttt ataatctcga agacaaccgt ccattgtttg gagatcggga caatacaatc
 900
 aaatacaact ttgaggaggt ttcagaggag cgtagaaatg gctatgcttg gttcggcaac
 960
 tggccggaag agctgatcca aaaggactat ccaaaatgga aaaaacaata caaaattcaa
 1020
 taa
 1023

<210> 64
 <211> 340
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(16)

<221> DOMAIN
 <222> (17)...(340)
 <223> Catalytic domain

<400> 64
 Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
 1 5 10 15
 Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
 20 25 30
 Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
 35 40 45
 Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Leu Leu Gln Gln Ile Lys
 50 55 60
 Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
 65 70 75 80
 Glu Ile Thr Glu Leu Ile Lys Ala Phe Lys Asp Thr Lys Asn Lys Ala

				85					90					95			
Tyr	Leu	Thr	Ala	Ala	Glu	Lys	Gly	Ile	Ala	Tyr	Ile	Leu	Ser	Ala	Gln		
			100					105					110				
Tyr	Glu	Asn	Gly	Gly	Phe	Pro	Gln	Tyr	Tyr	Pro	Asn	Lys	Leu	Tyr	Tyr		
		115					120					125					
Arg	Ala	Glu	Ile	Thr	Tyr	Asn	Asp	Asp	Ala	Met	Ile	Asn	Ala	Leu	Leu		
	130					135					140						
Val	Leu	Tyr	Lys	Val	Ala	Asn	Lys	Arg	Glu	Gly	Phe	Glu	Ala	Ile	Asn		
145					150					155					160		
Pro	Ile	Phe	Val	Ser	Lys	Ala	Gln	Lys	Ala	Val	Glu	Lys	Gly	Ile	Thr		
				165					170					175			
Cys	Ile	Leu	Lys	Thr	Gln	Val	Ile	Gln	Asp	Gly	Lys	Arg	Ser	Ile	Trp		
			180					185					190				
Ala	Ala	Gln	Tyr	Asp	Gln	Asn	Thr	Leu	Gln	Pro	Ala	Gln	Ala	Arg	Lys		
		195					200					205					
Phe	Glu	Pro	Ala	Ser	Leu	Ser	Thr	Ser	Glu	Ser	Val	Ser	Ile	Val	Arg		
	210					215					220						
Phe	Leu	Met	Leu	Gln	Pro	Ala	Thr	Thr	Glu	Ile	Lys	Gln	Ala	Ile	Glu		
225					230					235					240		
His	Ala	Ile	Gln	Trp	Phe	Glu	Gln	His	Asp	Ile	Glu	Gly	Tyr	Arg	Phe		
				245					250					255			
Asp	Arg	Ile	Gln	Asp	Arg	Val	Thr	Gly	Lys	Tyr	Gln	Arg	Gln	Leu	Val		
			260					265					270				
Ala	Asp	Arg	Thr	Ser	Thr	Ile	Trp	Ala	Arg	Phe	Tyr	Asn	Leu	Glu	Asp		
	275						280					285					
Asn	Arg	Pro	Leu	Phe	Gly	Asp	Arg	Asp	Asn	Thr	Ile	Lys	Tyr	Asn	Phe		
	290					295					300						
Glu	Glu	Val	Ser	Glu	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Phe	Gly	Asn		
305					310					315					320		
Trp	Pro	Glu	Lys	Leu	Ile	Gln	Lys	Asp	Tyr	Pro	Lys	Trp	Lys	Lys	Gln		
				325					330					335			
Tyr	Lys	Ile	Gln														
			340														

<210> 65
 <211> 1311
 <212> DNA
 <213> Bacteria

<400> 65
 gtgaaccgac gtacccgcct gggagcggtc gccgcgaccg ccctcgccct gacggtcacc
 60
 gccccgcggc ccggtgcca cgccgccgt cccacgccg cgccacgcc ggtcgccgat
 120
 ccggtcgcgc ccacgtgcc cgccggcgac ggctgggct ccgaggggac cggcacgacc
 180
 ggtggggccg ccgccgaggc ctcccgggtc ttcaccgtcg ccacctggga ggagttccg
 240
 gccgcgctcg cggtgcccgg ctccgagccc aggatcgta agtggtggg cacgctgaac
 300
 gccaccgccg ccggtcgcgc cgcttcgag gcgcccgggt acgacttcgc ccgctacctc
 360
 gccgactacg acccggccgt gtgggggtac gagaaggagg tcagcgccc gcaggaggag
 420
 ctgcgggcgc cgtccgcgac cgcgagggc caggccatca aggtcaaggt gccggcgaac
 480
 accacgatcg tcggggtcgc caggcacgcg gggatcacgc gcggcagcct ccagggtgcg
 540
 ggcgtcgaca acgtcgtggt ccgcaacctg acgctggaga gcccgtcga ctgcttcccc
 600
 cagtgggacc cgaccgacgc cgcgaccggg gcgtggaact ccgagtacga cagcctcgtc

660
 gtgtacggct ccacccatgt ctggatcgac cacaacacct tcaccgacgg cgcccacccg
 720
 gacagttcgc tggcctcgta ctacggcgag gtctaccagc agcacgacgg cgaactggac
 780
 gtcgtgcggg gcgcggacct cgtcacggtc tcgtggaacg ccttcaccga ccacgacaag
 840
 accctgatga tcggcaacag cgacagcgcg ggcgccaccg accgggggcaa gctgcggggtc
 900
 accctgcacc acaacctgtt cgagaacgtc gtcgagcggg cgccccgggt caggttcggg
 960
 caggtcgacg cgtacaacaa ccacttcgtc gtgccgagtt cggcctacgc gtacagcctg
 1020
 ggcgtcgggc aggagtccca gctcttcgcg gagaagaacg cgttcaccct cgccgggggc
 1080
 gtgccggccg ggaagatcct caagaagtgg aaggacgcgc ccgtcaccac cgtcggcaac
 1140
 tacgtgaacg gcaggccggt cgacctgctc gccgtccaca acaccagtt cccggaggag
 1200
 cagttgcggg ccgacgcggg ctggaccccc gtcctgcgca ccagggtcga ccaccgagg
 1260
 gccgtccccg cgctcgtcga ccaccgcgcg ggcgccggcc gctcctgctg a
 1311

<210> 66
 <211> 436
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(28)

<221> DOMAIN
 <222> (29)...(436)
 <223> Catalytic domain

<400> 66
 Met Asn Arg Arg Thr Arg Leu Gly Ala Val Ala Ala Thr Ala Leu Ala
 1 5 10 15
 Leu Thr Val Thr Ala Pro Ala Ala Gly Ala His Ala Ala Ala Pro His
 20 25 30
 Ala Ala Pro Arg Pro Val Ala Asp Pro Ala Arg Ala Thr Leu Pro Ala
 35 40 45
 Gly Asp Gly Trp Ala Ser Glu Gly Thr Gly Thr Thr Gly Gly Ala Ala
 50 55 60
 Ala Glu Ala Ser Arg Val Phe Thr Val Ala Thr Trp Glu Glu Phe Arg
 65 70 75 80
 Ala Ala Leu Ala Val Pro Gly Ser Glu Pro Arg Ile Val Lys Val Val
 85 90 95
 Gly Thr Leu Asn Ala Thr Ala Ala Gly Cys Gly Ala Phe Glu Ala Pro
 100 105 110
 Gly Tyr Asp Phe Ala Arg Tyr Leu Ala Asp Tyr Asp Pro Ala Val Trp
 115 120 125
 Gly Tyr Glu Lys Glu Val Ser Gly Pro Gln Glu Glu Leu Arg Ala Ala
 130 135 140
 Ser Ala Thr Ala Gln Gly Gln Ala Ile Lys Val Lys Val Pro Ala Asn
 145 150 155 160
 Thr Thr Ile Val Gly Val Gly Arg His Ala Gly Ile Thr Gly Gly Ser
 165 170 175

Leu Gln Val Gln Gly Val Asp Asn Val Val Val Arg Asn Leu Thr Leu
 180 185 190
 Glu Ser Pro Leu Asp Cys Phe Pro Gln Trp Asp Pro Thr Asp Gly Ala
 195 200 205
 Thr Gly Ala Trp Asn Ser Glu Tyr Asp Ser Leu Val Val Tyr Gly Ser
 210 215 220
 Thr His Val Trp Ile Asp His Asn Thr Phe Thr Asp Gly Ala His Pro
 225 230 235 240
 Asp Ser Ser Leu Pro Ser Tyr Tyr Gly Glu Val Tyr Gln Gln His Asp
 245 250 255
 Gly Glu Leu Asp Val Val Arg Gly Ala Asp Leu Val Thr Val Ser Trp
 260 265 270
 Asn Ala Phe Thr Asp His Asp Lys Thr Leu Met Ile Gly Asn Ser Asp
 275 280 285
 Ser Ala Gly Ala Thr Asp Arg Gly Lys Leu Arg Val Thr Leu His His
 290 295 300
 Asn Leu Phe Glu Asn Val Val Glu Arg Ala Pro Arg Val Arg Phe Gly
 305 310 315 320
 Gln Val Asp Ala Tyr Asn Asn His Phe Val Val Pro Ser Ser Ala Tyr
 325 330 335
 Ala Tyr Ser Leu Gly Val Gly Gln Glu Ser Gln Leu Phe Ala Glu Lys
 340 345 350
 Asn Ala Phe Thr Leu Ala Gly Gly Val Pro Ala Gly Lys Ile Leu Lys
 355 360 365
 Lys Trp Lys Asp Ala Pro Val Thr Thr Val Gly Asn Tyr Val Asn Gly
 370 375 380
 Arg Pro Val Asp Leu Leu Ala Val His Asn Thr Gln Phe Pro Glu Glu
 385 390 395 400
 Gln Leu Arg Ala Asp Ala Gly Trp Thr Pro Val Leu Arg Thr Arg Val
 405 410 415
 Asp His Pro Arg Ala Val Pro Ala Leu Val Asp His Arg Ala Gly Ala
 420 425 430
 Gly Arg Ser Cys
 435

<210> 67
 <211> 1995
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 67
 atgaaaaatt caaaaactgt ttttactgca caaaaaaac tcatgcactc ttgcattgcc
 60
 gccgctatcg gcttggcgat aagttcaggt gcttggtcag cttgtactta cactgtcacc
 120
 aataattggg gttctggctt caccggtgaa atcaaagtta ccaacaacac atcatcggct
 180
 gtaaatgggt ggtctgtgtc ttggcaggaa tcaggcgcac cagtcaccaa ctcatggaac
 240
 gcaactctga gcggatcaaa tccttatacg gcagccgcct taggttggaa tgcaactctc
 300
 gcacccggtg cttctgccag ttttggcttt caagcaaatg gcaactgctag cgcacctaaa
 360
 gtgaatggca ctttatgtgg aacagctact tcatcaacac ctgcgtcatc cagcagtgtt
 420
 gcgagttcgg ttaaatcaag cgacccggtt tcgtccagca gtaaatcatc cagctcaatc
 480
 actgtgagta gtagttctat cgccagcagc agcgcaccaa gtgtttcttc attaacaatt

540
 caggaagagc aagctggctt ctgtcgtgtt gatggcattg caacagaaag caccaacacc
 600
 ggctttaccg gcaacggcta taccaatgca aacaacgcac aaggtgcagc gattgaatgg
 660
 gcggtaaaatg caccgagcag tggccgctac aactcacat tccgttttgc aaatggcggc
 720
 actgcagcac gcaatggttc actgttaatt aacggcggta gcaatggtaa ctacaccgtg
 780
 gatttaccac taaccggcgc atgggcgact tggcaaacag cgactgtaga aatcgatttg
 840
 gtacaaggca ccaacacgct gaaactttct gcattaaccg cagatggctt agctaatac
 900
 gattcattaa aaattgatgg caaccaaccg aaagcaggca cttgcagcaa tacatcaagc
 960
 agtgttgcca gcagttcttc atccgttaaa tccagttcaa gttcttcac aagctcatcc
 1020
 accactgcaa aaatgctgac tcttgatggc aaccccgccg caagttgggt caacaaatcc
 1080
 agaaccaa at ggaatagcag tcgtgcggac attgtgtgt cttaccagca agctaacggc
 1140
 ggctggccaa aaaatctgga ttacaactca gtaagcgag gtaatgggtg tagcgacagc
 1200
 ggcatatcg acaacggcgc aaccatcacg gaaatggtt atctcgaga agtttataaa
 1260
 aacgggggca atacaaaata tcgcatgca gtacgtaaag cggcaaactt tattgtgagt
 1320
 tcgcaataca gactgggtgc gttaccacaa ttttaccat tgaaagggtg ttatgcagat
 1380
 cagccacct ttaacgataa cggcatggct tacgcattaa cggatttga ttttgcggtg
 1440
 aacaaacgtg cgccgtttga taacgatga ttttctgat cagaccgcgc aaaattcaaa
 1500
 actgccgtga ccaaaggtat tgattacatt ttgaaagccc aatggaaaca aaatggaaaa
 1560
 ctaccgcat ggtgtgcgca acacggagca aacgactatc aacaaaaagc ggcgctgct
 1620
 tatgagttag tatctttaag cggcagcgaa tccgttggca tcacgcttt cctgatgacc
 1680
 caaccacaaa ctgcgcaaat cgaagcagcg gttaaagccg gtgtaaaactg gttcgctagc
 1740
 ccgaatacat acttggttaa ttacacctac gactcgtcaa aagcctctac caatccgatt
 1800
 gtgtacaaat ccggcagcag aatgtggtat cgcttctac atctgaacac caatcgcgga
 1860
 ttcttttagtg atcgcgatgg cagcaaattc tatgacatca ctcaaagtgc tgaagaacgt
 1920
 cgcaccggct acagctgggg cggttcttac ggtgaatcga ttatcagctt cgcgcaaaaa
 1980
 gtgggttatc tctaa
 1995

<210> 68
 <211> 664
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample
 <221> SIGNAL

<222> (1)...(32)

<221> BINDING

<222> (33)...(126)

<223> Carbohydrate binding module

<221> BINDING

<222> (184)...(307)

<223> Carbohydrate binding module

<221> DOMAIN

<222> (308)...(664)

<223> Catalytic domain

<400> 68

Met	Lys	Asn	Ser	Lys	Thr	Val	Phe	Thr	Ala	Gln	Lys	Lys	Leu	Met	His
1				5					10					15	
Ser	Cys	Ile	Ala	Ala	Ala	Ile	Gly	Leu	Ala	Ile	Ser	Ser	Gly	Ala	Trp
			20					25					30		
Ser	Ala	Cys	Thr	Tyr	Thr	Val	Thr	Asn	Asn	Trp	Gly	Ser	Gly	Phe	Thr
		35				40					45				
Gly	Glu	Ile	Lys	Val	Thr	Asn	Asn	Thr	Ser	Ser	Ala	Val	Asn	Gly	Trp
	50					55					60				
Ser	Val	Ser	Trp	Gln	Glu	Ser	Gly	Ala	Ser	Val	Thr	Asn	Ser	Trp	Asn
65				70					75					80	
Ala	Thr	Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Ala	Ala	Ala	Leu	Gly	Trp
			85					90					95		
Asn	Ala	Thr	Leu	Ala	Pro	Gly	Ala	Ser	Ala	Ser	Phe	Gly	Phe	Gln	Ala
			100					105				110			
Asn	Gly	Thr	Ala	Ser	Ala	Pro	Lys	Val	Asn	Gly	Thr	Leu	Cys	Gly	Thr
	115					120						125			
Ala	Thr	Ser	Ser	Thr	Pro	Ala	Ser	Ser	Ser	Ser	Val	Ala	Ser	Ser	Val
	130					135					140				
Lys	Ser	Ser	Ala	Pro	Val	Ser	Ser	Ser	Ser	Lys	Ser	Ser	Ser	Ser	Ile
145				150						155					160
Thr	Val	Ser	Ser	Ser	Ser	Ile	Ala	Ser	Ser	Ser	Ala	Pro	Ser	Val	Ser
			165					170						175	
Ser	Leu	Thr	Ile	Gln	Glu	Glu	Gln	Ala	Gly	Phe	Cys	Arg	Val	Asp	Gly
		180						185					190		
Ile	Ala	Thr	Glu	Ser	Thr	Asn	Thr	Gly	Phe	Thr	Gly	Asn	Gly	Tyr	Thr
	195					200					205				
Asn	Ala	Asn	Asn	Ala	Gln	Gly	Ala	Ala	Ile	Glu	Trp	Ala	Val	Asn	Ala
	210				215					220					
Pro	Ser	Ser	Gly	Arg	Tyr	Thr	Leu	Thr	Phe	Arg	Phe	Ala	Asn	Gly	Gly
225				230					235					240	
Thr	Ala	Ala	Arg	Asn	Gly	Ser	Leu	Leu	Ile	Asn	Gly	Gly	Ser	Asn	Gly
			245					250					255		
Asn	Tyr	Thr	Val	Asp	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln
		260						265					270		
Thr	Ala	Thr	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Thr	Asn	Thr	Leu	Lys
	275					280						285			
Leu	Ser	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys
	290				295					300					
Ile	Asp	Gly	Asn	Gln	Pro	Lys	Ala	Gly	Thr	Cys	Ser	Asn	Thr	Ser	Ser
305				310					315					320	
Ser	Val	Ala	Ser	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ser	Ser	Ser	Ser
			325						330					335	
Ser	Ser	Ser	Ser	Thr	Thr	Ala	Lys	Met	Leu	Thr	Leu	Asp	Gly	Asn	Pro
		340				345						350			
Ala	Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg
	355					360						365			

Ala Asp Ile Val Leu Ser Tyr Gln Gln Ala Asn Gly Gly Trp Pro Lys
 370 375 380
 Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser
 385 390 395 400
 Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala
 405 410 415
 Glu Val Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg
 420 425 430
 Lys Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu
 435 440 445
 Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe
 450 455 460
 Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val
 465 470 475 480
 Asn Lys Arg Ala Pro Phe Asp Asn Asp Val Phe Ser Asp Ala Asp Arg
 485 490 495
 Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Ile Asp Tyr Ile Leu Lys
 500 505 510
 Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His
 515 520 525
 Gly Ala Asn Asp Tyr Gln Pro Lys Ala Ala Arg Ala Tyr Glu Leu Val
 530 535 540
 Ser Leu Ser Gly Ser Glu Ser Val Gly Ile Ile Ala Phe Leu Met Thr
 545 550 555 560
 Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
 565 570 575
 Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
 580 585 590
 Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
 595 600 605
 Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
 610 615 620
 Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
 625 630 635 640
 Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
 645 650 655
 Phe Ala Gln Lys Val Gly Tyr Leu
 660

<210> 69
 <211> 1035
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 69
 atggcgcgtt tggtccggtg cgtgtgtgcc agcctgggag gatgggccgc ggttctggcc
 60
 gccgcggcgg gcccgattg gtcccgctg ctgcgcgaac cggacccttg gtttcgcagt
 120
 ccggcggggc aacaggcgtt gacgaacgtt ttgtcctggc agagcgcgac aggcgcctgg
 180
 ccgaaaaacc tggacaccac ccgcgagccg cgtcggcagg attccgcccc gcccgagggc
 240
 actttcgaca acggcgccac caccggcgag ttgcggtttc tggcgcgggc gtttgcggcc
 300
 accggcgatc cgcgctgcga agccgcggtg ctccgggggc tggacggcat cctcgcggcc
 360
 cagcttccca gcggcggctg gccgcagtgt catcctccgc gcgcgcctta tcagcgccac

420
 atcaccttca acgacggtgt catggtgcgc atcctggagc tgctgcgcga gatagaccgc
 480
 gcgccggagt ttcgctgggt ggacgaggcg cggcgcgcgcg gggcgcgcgcg ggccttcact
 540
 cgcgggctgg agtgcctcct gcgctgccag gtggtcgtcg agggcagact caccgtgtgg
 600
 tgtgcccagc atgacgcgga gaactttcaa ccgcgaccgg cacgcgccta cgaactggaa
 660
 tcgctcagcg gcgcggaaaag cgccggcatc ctggtgttcc tcatgagcct ggagccgcca
 720
 accccggaga tcgcgcgcgc ggtcgaggcc ggggcggcct ggttttcggc ggtaaagctt
 780
 gaagggttcc gtctcgaacg aacggccgac gacgcgcggg tggtggaaga gccgggcgcg
 840
 ccgcgcgtct gggcgcggtt ctacgagatc gggaccaatc gcccacatct tgccggtcgc
 900
 gacggtgtca agaagtacgc cctgagcgag atcgagcggg aacgccgggt cggctatgcg
 960
 tggtagggcg cctgggggtga accggtcgcc cgccattatg cccagtggcg ggagcgttac
 1020
 gggacgcaga aatga
 1035

<210> 70
 <211> 344
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(22)

<221> DOMAIN
 <222> (23)...(344)
 <223> Catalytic domain

<400> 70
 Met Ala Arg Leu Phe Arg Cys Val Cys Ala Ser Leu Gly Gly Trp Ala
 1 5 10 15
 Ala Val Leu Ala Ala Ala Ala Gly Pro Asp Trp Ser Arg Leu Leu Ala
 20 25 30
 Gln Pro Asp Pro Trp Phe Arg Ser Pro Ala Gly Gln Gln Ala Val Thr
 35 40 45
 Asn Val Leu Ser Trp Gln Ser Ala Thr Gly Ala Trp Pro Lys Asn Leu
 50 55 60
 Asp Thr Thr Arg Glu Pro Arg Arg Gln Asp Ser Ala Pro Pro Glu Gly
 65 70 75 80
 Thr Phe Asp Asn Gly Ala Thr Thr Gly Glu Leu Arg Phe Leu Ala Arg
 85 90 95
 Ala Phe Ala Ala Thr Gly Asp Pro Arg Cys Glu Ala Ala Val Leu Arg
 100 105 110
 Gly Leu Asp Gly Ile Leu Ala Ala Gln Leu Pro Ser Gly Gly Trp Pro
 115 120 125
 Gln Cys His Pro Pro Arg Ala Pro Tyr Gln Arg His Ile Thr Phe Asn
 130 135 140
 Asp Gly Val Met Val Arg Ile Leu Glu Leu Leu Arg Glu Ile Asp Arg
 145 150 155 160
 Ala Pro Glu Phe Arg Trp Val Asp Glu Ala Arg Arg Ala Arg Val Arg

				165					170					175			
Ala	Ala	Phe	Thr	Arg	Gly	Leu	Glu	Cys	Leu	Leu	Arg	Cys	Gln	Val	Val		
			180					185					190				
Val	Glu	Gly	Arg	Leu	Thr	Val	Trp	Cys	Ala	Gln	His	Asp	Ala	Glu	Asn		
		195					200					205					
Phe	Gln	Pro	Arg	Pro	Ala	Arg	Ala	Tyr	Glu	Leu	Glu	Ser	Leu	Ser	Gly		
	210					215					220						
Ala	Glu	Ser	Ala	Gly	Ile	Leu	Val	Phe	Leu	Met	Ser	Leu	Glu	Pro	Pro		
225				230				235						240			
Thr	Pro	Glu	Ile	Ala	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ala	Trp	Phe	Ser		
			245					250						255			
Ala	Val	Lys	Leu	Glu	Gly	Phe	Arg	Leu	Glu	Arg	Thr	Ala	Asp	Asp	Ala		
		260						265					270				
Arg	Val	Val	Glu	Glu	Pro	Gly	Ala	Pro	Pro	Leu	Trp	Ala	Arg	Phe	Tyr		
		275				280						285					
Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Ala	Gly	Arg	Asp	Gly	Val	Lys		
	290					295					300						
Lys	Tyr	Ala	Leu	Ser	Glu	Ile	Glu	Arg	Glu	Arg	Arg	Val	Gly	Tyr	Ala		
305					310					315				320			
Trp	Tyr	Gly	Ala	Trp	Gly	Glu	Pro	Val	Ala	Arg	His	Tyr	Ala	Gln	Trp		
			325					330						335			
Arg	Glu	Arg	Tyr	Gly	Thr	Gln	Lys										
			340														

<210> 71
 <211> 1038
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 71
 gtgactcgtg tcgcccttgc gatggggcctt gttgcatggg ttccggcgct cgcttcagct
 60
 gggcccgcgt catatttgca gaagccggac gactgggttcg ccagtcccga ggccagggca
 120
 atcgccgcga acgtactcgc gcatcaggcc gatctcggcg ggtggccgaa gaacatcgac
 180
 acaacgaagc cgttcaccgg cgaccggacg caaatcaaac cgaccttcga taacagcgcg
 240
 acaaccgacg agctccgggt tctggcgcg atccacaacg cgactcgca cgagaagtag
 300
 cgcaccgcgt tcgagaagg gctcgattac atcttgaaag cacaatacgc aaacggcggt
 360
 tggccgcagt cgcacccgcc cggcaccggc taccaccggc acatcacctt caacgacaat
 420
 gccatggtcc gtttgatgga gctcgtgcgc gaagtcgca cctcgaatcg gtacgacttc
 480
 ctggacgccg accgccgcaa ggcctgccgc gccgctttcg atcgcgcat cgaatgcac
 540
 ctgaagtgcc agatcaaggt cgacagtaag ctgacggcat ggtgcgcca gcacgacgag
 600
 aaggacctcg ctccccggcc ggcgcgacc tacgagctcg tctcactcag cggctcggag
 660
 tcggtcggga tcgtccgcct actcatgagc ctcgatcgac caagcccga ggtcgtcgg
 720
 gccatcgacg gcgcggtcgc gtggttcag tcggcgaagc tcgaaggcac caaggtcgtt
 780
 gtcgagcgcg acccgaagta tccggggcgc cggaacgcg tgggtggtgaa ggatccaaag
 840

gcaccgccac tctgggcgcg cttctacgaa atcggcacga atcgcccat cttctccgac
 900
 cgcgacggca tcaagaagta cgcgctcgcc gagatcggcc ccgaacggcg gaatggctat
 960
 gcctggtatg gcacctggcc gcgcgacctg ctggagaagg aatacccagg gtggaaaaag
 1020
 aagctggccc ggccgtga
 1038

<210> 72
 <211> 345
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(20)

<221> DOMAIN
 <222> (21)...(345)
 <223> Catalytic domain

<400> 72
 Met Thr Arg Val Ala Leu Ala Met Gly Leu Val Ala Trp Val Pro Ala
 1 5 10 15
 Leu Ala Ser Ala Gly Pro Ala Ala Tyr Leu Gln Lys Pro Asp Asp Trp
 20 25 30
 Phe Ala Ser Pro Glu Ala Arg Ala Ile Ala Ala Asn Val Leu Ala His
 35 40 45
 Gln Ala Asp Leu Gly Gly Trp Pro Lys Asn Ile Asp Thr Thr Lys Pro
 50 55 60
 Phe Thr Gly Asp Arg Thr Gln Ile Lys Pro Thr Phe Asp Asn Ser Ala
 65 70 75 80
 Thr Thr Asp Glu Leu Arg Phe Leu Ala Arg Ile His Asn Ala Thr Arg
 85 90 95
 Asp Glu Lys Tyr Arg Thr Ala Phe Glu Lys Gly Leu Asp Tyr Ile Leu
 100 105 110
 Lys Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Ser His Pro Pro Gly
 115 120 125
 Thr Gly Tyr His Arg His Ile Thr Phe Asn Asp Asn Ala Met Val Arg
 130 135 140
 Leu Met Glu Leu Val Arg Glu Val Ala Thr Ser Asn Arg Tyr Asp Phe
 145 150 155 160
 Leu Asp Ala Asp Arg Arg Lys Ala Cys Arg Ala Ala Phe Asp Arg Gly
 165 170 175
 Ile Glu Cys Ile Leu Lys Cys Gln Ile Lys Val Asp Ser Lys Leu Thr
 180 185 190
 Ala Trp Cys Ala Gln His Asp Glu Lys Asp Leu Ala Pro Arg Pro Ala
 195 200 205
 Arg Thr Tyr Glu Leu Val Ser Leu Ser Gly Ser Glu Ser Val Gly Ile
 210 215 220
 Val Arg Leu Leu Met Ser Leu Asp Arg Pro Ser Pro Glu Val Ala Arg
 225 230 235 240
 Ala Ile Asp Gly Ala Val Ala Trp Phe Gln Ser Ala Lys Leu Glu Gly
 245 250 255
 Thr Lys Val Val Glu Arg Asp Pro Lys Tyr Pro Gly Gly Arg Glu
 260 265 270
 Arg Val Val Val Lys Asp Pro Lys Ala Pro Pro Leu Trp Ala Arg Phe
 275 280 285

Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Ser	Asp	Arg	Asp	Gly	Ile
	290					295					300				
Lys	Lys	Tyr	Ala	Leu	Ala	Glu	Ile	Gly	Pro	Glu	Arg	Arg	Asn	Gly	Tyr
305					310					315					320
Ala	Trp	Tyr	Gly	Thr	Trp	Pro	Arg	Asp	Leu	Leu	Glu	Lys	Glu	Tyr	Pro
			325						330					335	
Gly	Trp	Lys	Lys	Lys	Leu	Ala	Arg	Pro							
		340						345							

<210> 73
 <211> 1221
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 73
 atgctcacca aaacatcact acttattgca ttgctaggca gttgttgtat cgcaccatta
 60
 catgcgga caccagcaag caatgcaccg acaaccaatg catcaattcc gctacagcaa
 120
 actgagagcg atgctgccgc ctggaaaaat tatctcgcca aatccaacga gttgagcaaa
 180
 gcagaccagg cgcagctcaa agccgagctg aaaaaactcg ggcaaaaaac cgcgagtttg
 240
 cctgagtaca ccaaagaatt tggttttgaa gtgaagcagt catctgagtg gtttaaaagc
 300
 actgaaggta aacgagtgat ggatattatc ctatcgtttc aaactccttc tggcggctgg
 360
 tcaaaacgca ctgacatgag caaagcgccg cgcaaaccgc gccaggcatt tgggtgtgaa
 420
 aaaaattaca tccccacctt tgataatggc gcgaccagca cacaattaat gctactggca
 480
 caggcgcatc aagccactgg cgataaacgc tacagcgatg catttgcgcg cgggcttgaa
 540
 tttatcatca ccgctcaata tccaatggc ggctggccac aaaattttcc attggttggc
 600
 aagtatcacg atcacatcac ttacaacgat gccctgatgc gcgatttaat ggtagtgcta
 660
 cacaagggtg ccatggccaa ggatgaattt gcctttgtat ccaaggcgca gcaacaggcc
 720
 gcacaagcga gcctcgaacg cgcgctggac tgcgttttga aaaccaggt gatggccaat
 780
 ggccaattaa ctatatgggg tgcgcagcac gatgccaaaa ccttaaaacc cgccaaagcg
 840
 cgcgcctatg aaatgatttc actcaccagt tctgaaagcg tgtggatgct cgatttttta
 900
 atggatttgc aacagcccag cgctgacatt attaaatccg tgcacgcggc tgccgcttgg
 960
 tatgagcaaa ataaaattat cggaataaac tggaccgggg gcgacacagt tctgaaagac
 1020
 gataaggatg caccgccaat ctgggcgcgt ttttatgaga taggtacgaa caaaccctg
 1080
 tttggcgacc gcgatgactc tgtccattac gatctggcaa aggtatcgga agagcgccgc
 1140
 acgggttatg cctggtacac aacctaccc aatcaggat taaaaaagta cgcgcgctgg
 1200
 gctaaacaat atccgcaata a
 1221

<210> 74
<211> 406
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(406)
<223> Catalytic domain

<400> 74

Met	Leu	Thr	Lys	Thr	Ser	Leu	Leu	Ile	Ala	Leu	Leu	Gly	Ser	Cys	Cys	
1				5					10					15		
Ile	Ala	Pro	Leu	His	Ala	Asp	Thr	Pro	Ala	Ser	Asn	Ala	Pro	Thr	Thr	
			20					25					30			
Asn	Ala	Ser	Ile	Pro	Leu	Gln	Gln	Thr	Ala	Ser	Asp	Ala	Ala	Ala	Trp	
		35				40						45				
Lys	Asn	Tyr	Leu	Ala	Lys	Ser	Asn	Glu	Leu	Arg	Lys	Ala	Asp	Gln	Ala	
	50					55					60					
Gln	Leu	Lys	Ala	Glu	Leu	Lys	Lys	Leu	Gly	Gln	Lys	Thr	Ala	Ser	Leu	
65				70					75						80	
Pro	Glu	Tyr	Thr	Lys	Glu	Phe	Gly	Phe	Glu	Val	Lys	Gln	Ser	Ser	Glu	
				85				90						95		
Trp	Phe	Lys	Ser	Thr	Glu	Gly	Lys	Arg	Val	Met	Asp	Ile	Ile	Leu	Ser	
			100					105					110			
Phe	Gln	Thr	Pro	Ser	Gly	Gly	Trp	Ser	Lys	Arg	Thr	Asp	Met	Ser	Lys	
		115					120					125				
Ala	Pro	Arg	Lys	Pro	Gly	Gln	Ala	Phe	Gly	Val	Glu	Lys	Asn	Tyr	Ile	
	130					135					140					
Pro	Thr	Phe	Asp	Asn	Gly	Ala	Thr	Ser	Thr	Gln	Leu	Met	Leu	Leu	Ala	
145					150					155					160	
Gln	Ala	His	Gln	Ala	Thr	Gly	Asp	Lys	Arg	Tyr	Ser	Asp	Ala	Phe	Ala	
				165					170					175		
Arg	Gly	Leu	Glu	Phe	Ile	Ile	Thr	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp	
			180					185					190			
Pro	Gln	Asn	Phe	Pro	Leu	Val	Gly	Lys	Tyr	His	Asp	His	Ile	Thr	Tyr	
		195					200					205				
Asn	Asp	Ala	Leu	Met	Arg	Asp	Leu	Met	Val	Val	Leu	His	Lys	Val	Ala	
	210					215					220					
Met	Ala	Lys	Asp	Glu	Phe	Ala	Phe	Val	Ser	Lys	Ala	Gln	Gln	Gln	Ala	
225					230					235					240	
Ala	Gln	Ala	Ser	Leu	Glu	Arg	Ala	Leu	Asp	Cys	Val	Leu	Lys	Thr	Gln	
				245					250					255		
Val	Met	Ala	Asn	Gly	Gln	Leu	Thr	Ile	Trp	Gly	Ala	Gln	His	Asp	Ala	
			260					265					270			
Lys	Thr	Leu	Lys	Pro	Ala	Lys	Ala	Arg	Ala	Tyr	Glu	Met	Ile	Ser	Leu	
		275					280					285				
Thr	Ser	Ser	Glu	Ser	Val	Trp	Met	Leu	Asp	Phe	Leu	Met	Asp	Leu	Gln	
	290					295					300					
Gln	Pro	Ser	Ala	Asp	Ile	Ile	Lys	Ser	Val	His	Ala	Ala	Ala	Ala	Trp	
305					310					315					320	
Tyr	Glu	Gln	Asn	Lys	Ile	Ile	Gly	Lys	Thr	Trp	Thr	Arg	Gly	Asp	Thr	
				325					330				335			
Val	Leu	Lys	Asp	Asp	Lys	Asp	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	
			340				345					350				
Glu	Ile	Gly	Thr	Asn	Lys	Pro	Leu	Phe	Gly	Asp	Arg	Asp	Asp	Ser	Val	

	355		360		365										
His	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Glu	Glu	Arg	Arg	Thr	Gly	Tyr	Ala
	370					375					380				
Trp	Tyr	Thr	Thr	Ser	Pro	Asn	Gln	Val	Leu	Lys	Lys	Tyr	Ala	Arg	Trp
385					390					395					400
Ala	Lys	Gln	Tyr	Pro	Gln										
				405											

<210> 75
 <211> 1767
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 75
 atgaccacaa cccgccgcac tatcctgaaa gccgccgcca gcgccggcgc gatcgccagc
 60
 accggctggc ccgccttggc cgccgcacag gccgcgcaag ccgccgaccc gtgggcccgc
 120
 gccagcaga tcatcgaccg cttcgccaag ccgctcagct tcccgaacag ggacttcccg
 180
 atcaccgagt tcggcgccaa accctgcaag ctggtcaaag ccagggcct ggtcgaagta
 240
 agagtcaaag gcgaactcga aacgccagca ccgcaagcgc cggacgccta cccggcaatc
 300
 aaagccgcca tcgccgcagc gagcaaggcc ggaggagggc gcgtgctgat cccggccggc
 360
 aactggtact gcaagggccc tatcgtgctg ctgtcgaacg tgcacgtgca ccttgccaag
 420
 ggcgcgcaag tctacttcag cgccaacgcc aaggacttcg cccgcgacgg cgactacgac
 480
 tgccggcgcca acggcaagct ggtgctctcg cgctggcaag gcaacgattg cctgaacttc
 540
 tcgcccattg tctacgcgcg cgggcaaaag aatatcgcca ttaccggcga agactggacc
 600
 agcatcctga acggccaggc cggcgtggcg ttcgaagacg gcagcggcaa tggctggtgg
 660
 ggcatgaacc ccgccggcgc gccgcccggc agcaccacgc accagggcgc agccaatccg
 720
 aacaacgccg aggagccaat cgccagactg cccacgcgcc acgcgaactg gagcgccgac
 780
 gacaagtacc tgccgctgct gtccgaagcc ggcgtgcccg ccgagcgcgg cgtgttcggt
 840
 ctggggcact acctgcggcc gtcgatggtc gaattcgtcg actgcgggga tgtgctgatg
 900
 cagggtacc aggtcatcaa cacgccgttc tggattcatc acccggtcaa ctcacgcaac
 960
 attcacttct ccaaagtgcg catggaaagc atcggcccgga attcggacgg tttcgatccc
 1020
 gagtctcg acaccatcct ggtggacggc tgctgttca ataccggcga cgactgcac
 1080
 gccatcaa at ccggcaagaa ccgagactcg caatacggcc caacgcgcaa tatggtggtc
 1140
 cagaactgca tcatgaaccg cgccacggc ggcgttacgc tgggcagcga aatggcgggt
 1200
 ggcatcgagc atatctacgc gcagaaaatc gaattccgca acgcgttctg ggaccacgac
 1260
 ccgctgggca cggccatccg aatgaagacg aacatgaacc gcggcggcta ccttcgtcat
 1320

ttctacgtgc gcgacgtgac gctgccgaat ggcgtgcgta ccaagagcgg cttctacaag
 1380
 acgctgccgg gatctccgct ggcaggcaag gtctccacca gcggcggcgc tgttatcact
 1440
 atcgactgcg attacgcgcc gaatgacgac agcgtgcgcg tgcggccgcc gcaggtgtcg
 1500
 gacgtgcata tctcgaacgt ccgcgtcagc aatgtgaaaa cggccgaagg ctcgttctcc
 1560
 tgctaccagg ccatggtgct gctcggggccc gtggcgggcca gcttcaacgg cgcgcctggc
 1620
 acggccatcc tgccgatcac gaatgtcacc gtcagcgatt cggacttcgg cagccgcgc
 1680
 aacagcgcag agccctggtt cgcgttcaac gtgcaggggac tcaagctgcg caacgtgcgc
 1740
 atcgatggca aggagtacaa cgtatga
 1767

<210> 76
 <211> 588
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(34)
 <221> DOMAIN
 <222> (110)...(555)
 <223> Catalytic domain

<400> 76
 Met Thr Thr Thr Arg Arg Thr Ile Leu Lys Ala Ala Ala Ser Ala Gly
 1 5 10 15
 Ala Ile Ala Ser Thr Gly Trp Pro Ala Leu Ala Ala Ala Gln Ala Ala
 20 25 30
 Gln Ala Ala Asp Pro Trp Ala Arg Ala Gln Gln Ile Ile Asp Arg Phe
 35 40 45
 Ala Lys Pro Leu Ser Phe Pro Asn Arg Asp Phe Pro Ile Thr Glu Phe
 50 55 60
 Gly Ala Lys Pro Cys Lys Leu Val Lys Ala Gln Gly Leu Val Glu Val
 65 70 75 80
 Arg Val Lys Gly Glu Leu Glu Thr Pro Ala Pro Gln Ala Pro Asp Ala
 85 90 95
 Tyr Pro Ala Ile Lys Ala Ala Ile Ala Ala Ala Ser Lys Ala Gly Gly
 100 105 110
 Gly Arg Val Leu Ile Pro Ala Gly Asn Trp Tyr Cys Lys Gly Pro Ile
 115 120 125
 Val Leu Leu Ser Asn Val His Val His Leu Ala Lys Gly Ala Gln Val
 130 135 140
 Tyr Phe Ser Ala Asn Ala Lys Asp Phe Ala Arg Asp Gly Asp Tyr Asp
 145 150 155 160
 Cys Gly Ala Asn Gly Lys Leu Val Leu Ser Arg Trp Gln Gly Asn Asp
 165 170 175
 Cys Leu Asn Phe Ser Pro Met Val Tyr Ala Arg Gly Gln Lys Asn Ile
 180 185 190
 Ala Ile Thr Gly Glu Asp Trp Thr Ser Ile Leu Asn Gly Gln Ala Gly
 195 200 205
 Val Ala Phe Glu Asp Gly Ser Gly Asn Gly Trp Trp Gly Met Asn Pro
 210 215 220

Ala Gly Ala Pro Pro Gly Ser Thr Thr His Gln Gly Ala Ala Asn Pro
 225 230 235 240
 Asn Asn Ala Glu Glu Pro Ile Ala Arg Leu Pro Thr Arg His Ala Asn
 245 250 255
 Trp Ser Ala Asp Asp Lys Tyr Leu Pro Leu Leu Ser Glu Ala Gly Val
 260 265 270
 Pro Ala Glu Arg Arg Val Phe Gly Leu Gly His Tyr Leu Arg Pro Ser
 275 280 285
 Met Val Glu Phe Val Asp Cys Gly Asp Val Leu Met Gln Gly Tyr Gln
 290 295 300
 Val Ile Asn Thr Pro Phe Trp Ile His His Pro Val Asn Ser Arg Asn
 305 310 315 320
 Ile His Phe Ser Lys Val Arg Met Glu Ser Ile Gly Pro Asn Ser Asp
 325 330 335
 Gly Phe Asp Pro Glu Ser Cys Asp Thr Ile Leu Val Asp Gly Cys Leu
 340 345 350
 Phe Asn Thr Gly Asp Asp Cys Ile Ala Ile Lys Ser Gly Lys Asn Arg
 355 360 365
 Asp Ser Gln Tyr Gly Pro Thr Arg Asn Met Val Val Gln Asn Cys Ile
 370 375 380
 Met Asn Arg Gly His Gly Gly Val Thr Leu Gly Ser Glu Met Ala Gly
 385 390 395 400
 Gly Ile Glu His Ile Tyr Ala Gln Lys Ile Glu Phe Arg Asn Ala Phe
 405 410 415
 Trp Asp His Asp Pro Leu Gly Thr Ala Ile Arg Met Lys Thr Asn Met
 420 425 430
 Asn Arg Gly Gly Tyr Leu Arg His Phe Tyr Val Arg Asp Val Thr Leu
 435 440 445
 Pro Asn Gly Val Arg Thr Lys Ser Gly Phe Tyr Lys Thr Leu Pro Gly
 450 455 460
 Ser Pro Leu Ala Gly Lys Val Ser Thr Ser Gly Gly Ala Val Ile Thr
 465 470 475 480
 Ile Asp Cys Asp Tyr Ala Pro Asn Asp Asp Ser Val Arg Val Arg Pro
 485 490 495
 Pro Gln Val Ser Asp Val His Ile Ser Asn Val Arg Val Ser Asn Val
 500 505 510
 Lys Thr Ala Glu Gly Ser Phe Ser Cys Tyr Gln Ala Met Val Leu Leu
 515 520 525
 Gly Pro Val Ala Ala Ser Phe Asn Gly Ala Pro Gly Thr Ala Ile Leu
 530 535 540
 Pro Ile Thr Asn Val Thr Val Ser Asp Ser Asp Phe Gly Thr Pro Arg
 545 550 555 560
 Asn Ser Ala Glu Pro Trp Phe Ala Phe Asn Val Gln Gly Leu Lys Leu
 565 570 575
 Arg Asn Val Arg Ile Asp Gly Lys Glu Tyr Asn Val
 580 585

<210> 77
 <211> 2043
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 77
 atgaaaacct ccagagcaat ttttactaca tcaacacttt tacaccgcgc gcttatcgcg
 60
 gctagtgtca gcatggcaat gagttctgcc gcatggggcgg gttgtaccta taccgtcacc
 120
 aataattggg gctcaggatt taccggcgaa atcaaagtga ccaacaacac caccgccagc

180
gtgaacaatt ggtctgtgtc atggcaggaa tccggtgcgg ctatcaccaa cgcctggaat
240
gcaacgctca gtggctcaaa cccttacaca gccgtatccg ctggttgga tggcacactt
300
gcccccaatg catcggccac ttttggtttc caggcaaacg gttctgccgg tgcacctaaa
360
gtgaatggca gcttgtgcgg caccaacact tcatcaacac cggcatccag cagtgttgcc
420
agctcggtta aatcaagcgc gcccgatcgc tccagcagca gatcatccag ttcaatcgtc
480
atcactagca gctctttagc gagaagttct attgcctcca gcagctcact agttagtagc
540
tccagagcga gcagtagtgc gccaaagcgtt ttctctttta cgatccagga agagcaagcg
600
ggcttctgtc gtgttgatgg cattgcgaca gaaagcacca acaccggttt taccggcaat
660
ggctacacca atgcgaacaa cgcgcaaggc gcagcgattg aatgggcagt cagcgcacct
720
agcagtggcc gttatacagt agccttccgc ttcgccaatg gcggcacagc agcgcgcaac
780
ggctcgttgt taatcaatgg cggtagcaat ggtaattaca ctgtggagtt acccctgacc
840
ggcgcattgg caacctggca aattgccagc gtggaaattg atttagtgca aggcaataat
900
attttaaaac tctcggcggt aaccgctgac ggtttgcca atatcgactc attaaaaata
960
gacggcgcgc aaaccaaagc aggtacttgc agcactacat caagcagcag cgttgccagc
1020
agctcgtcgt ccgttaaadc cagcgcaagt tcttcttcga gttcatccac cgctgcaaaa
1080
atactgacat tagacggtaa cccggccgcc agctggttca acaaataccag gaccaagtgg
1140
aatagcagcc gcgccgatat tgtgttgtct taccagcaat ccaacggcgg ttggccaaaa
1200
aacctggatt acaactcagt gagcgaggc aatggcgagg gcgacagcgg caccatcgac
1260
aatggtgcaa ccattaccga aatggtttac ctcgctgaaa ttataaaaaa cggcggcaac
1320
accaaataac gcgatgcagt gcgcagagca gcaaactttt tagtgagctc gcaatacagc
1380
acaggcgcct tgccacaatt ttatccgttg aaaggcggct atgcggatca tgcgaccttt
1440
aacgataacg gcatggcgta cgcgttgacg gtattggatt tcgcagtaaa caaacgcgca
1500
ccgtttgata acgacatttt ctctgattct gatcgggcga aattcaaaac cgctgttgcc
1560
aaaggtgtgg attacatttt aaaagcgagc tggaaacaaa atggaaaact cactgcatgg
1620
tgtgcacaac acggtgctac ggattaccaa ccgaaaaaag cgcgcgctta tgaattggaa
1680
tcattgagtg gtagcgagtc ggtcggcatt ctgccttct tgatgaccca accacaaacc
1740
gcgcaaactc aagcggcggc caaggcgggt gtcaactggc tcgccagtcc aaatacttat
1800
ttggctaact acacttacga ttcatcaaaa gcgtctacca acccgattgt gtataaatcc
1860
ggaagcagaa tgtggtatcg cttctatgac ctgaacacca accgtgggtt ctttagtgat
1920
cgcgatggca gcaaattcta tgatatcacc caaatgtcag aagagcgtcg caccgggtat
1980

agctgggggtg gctcttacgg tgaatctatt atttccttcg cgcaaaaagt gggttatctg
 2040
 taa
 2043

<210> 78
 <211> 680
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(33)

<221> BINDING
 <222> (34)...(126)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (199)...(322)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (323)...(680)
 <223> Catalytic domain

<400> 78
 Met Lys Thr Ser Arg Ala Ile Phe Thr Thr Ser Thr Leu Leu His Arg
 1 5 10 15
 Ala Leu Ile Ala Ser Val Ser Met Ala Met Ser Ser Ala Ala Trp
 20 25 30
 Ala Gly Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
 35 40 45
 Gly Glu Ile Lys Val Thr Asn Asn Thr Thr Ala Ser Val Asn Asn Trp
 50 55 60
 Ser Val Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn
 65 70 75 80
 Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp
 85 90 95
 Asn Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala
 100 105 110
 Asn Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr
 115 120 125
 Asn Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys
 130 135 140
 Ser Ser Ala Pro Val Ser Ser Ser Ser Arg Ser Ser Ser Ile Ala
 145 150 155 160
 Ile Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser
 165 170 175
 Leu Val Ser Ser Ser Arg Ala Ser Ser Ser Ala Pro Ser Val Phe Ser
 180 185 190
 Phe Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile
 195 200 205
 Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn
 210 215 220
 Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro
 225 230 235 240
 Ser Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr
 245 250 255

Ala	Ala	Arg	Asn	Gly	Ser	Leu	Leu	Ile	Asn	Gly	Gly	Ser	Asn	Gly	Asn
			260					265					270		
Tyr	Thr	Val	Glu	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Ile
		275					280					285			
Ala	Ser	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu
	290					295					300				
Ser	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile
305					310					315					320
Asp	Gly	Ala	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ser	Thr	Thr	Ser	Ser	Ser
				325					330					335	
Ser	Val	Ala	Ser	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ser	Ser
			340					345					350		
Ser	Ser	Ser	Ser	Thr	Ala	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro
		355					360					365			
Ala	Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg
	370					375					380				
Ala	Asp	Ile	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys
385					390					395					400
Asn	Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser
				405					410					415	
Gly	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala
			420					425					430		
Glu	Ile	Tyr	Lys	Asn	Gly	Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg
		435					440					445			
Arg	Ala	Ala	Asn	Phe	Leu	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu
	450					455					460				
Pro	Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe
465					470					475					480
Asn	Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val
				485					490					495	
Asn	Lys	Arg	Ala	Pro	Phe	Asp	Asn	Asp	Ile	Phe	Ser	Asp	Ser	Asp	Arg
			500					505					510		
Ala	Lys	Phe	Lys	Thr	Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys
		515					520					525			
Ala	Gln	Trp	Lys	Gln	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys	Ala	Gln	His
	530					535					540				
Gly	Ala	Thr	Asp	Tyr	Gln	Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu
545					550					555					560
Ser	Leu	Ser	Gly	Ser	Glu	Ser	Val	Gly	Ile	Leu	Ala	Phe	Leu	Met	Thr
				565					570					575	
Gln	Pro	Gln	Thr	Ala	Gln	Ile	Glu	Ala	Val	Lys	Ala	Gly	Val	Asn	
			580					585				590			
Trp	Phe	Ala	Ser	Pro	Asn	Thr	Tyr	Leu	Ala	Asn	Tyr	Thr	Tyr	Asp	Ser
		595					600					605			
Ser	Lys	Ala	Ser	Thr	Asn	Pro	Ile	Val	Tyr	Lys	Ser	Gly	Ser	Arg	Met
	610					615					620				
Trp	Tyr	Arg	Phe	Tyr	Asp	Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp
625					630					635					640
Arg	Asp	Gly	Ser	Lys	Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg
				645					650					655	
Arg	Thr	Gly	Tyr	Ser	Trp	Gly	Gly	Ser	Tyr	Gly	Glu	Ser	Ile	Ile	Ser
			660					665					670		
Phe	Ala	Gln	Lys	Val	Gly	Tyr	Leu								
		675					680								

<210> 79
 <211> 1746
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 79

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120
atcctcgcac gcatcacacc acctcggttt ccgaaacgca ccttctatct caatcgattc
180
ggcgccaagg gcgatggagt cacagactgc accgcggctt ttcacgcgc gatcgatgaa
240
tgcaccaaag ccggcggttg gaaagtcgtc gtgcggcggt gcacttatct caccggcgcg
300
attcatttga agagcaacgt caacctcgaa gtctcggaag gcgcgacgat caagttcagt
360
caggaccgga aacactacct gcctgttgct ttctcgcggt gggaagggtg cgaagtcttc
420
aactactcgc ctttcattta cgcgttcgaa cagcgaaaca tcgcgatcac cggcaaaggc
480
acgctcgacg gacagagtga ttcggaacac tgggtggcgt ggaacggccg tccgcagtac
540
ggatggaatg aagggatgaa acagcagcgt cccgatcgca acgcgttggt cacaatggcg
600
gagaaaggcg tgccggtgcg cgagcgcac tttggcgaag gtcattattt gagggccgag
660
ttcattcagc cgtaccgctg ccagaacgtg ctgatccagg gcgtgacgat tcggaactcg
720
ccgatgtggg agattcatcc ggtgttgctc cgcaacgtga ctattcacga cgtgcacatc
780
gatagtcatg gaccaaacia cgacggctgc aatcccgaat cgtgcagcga cgtgttgatt
840
aaggatagct acttcgatac cggcgacgac tgcacgcga tcaaacggg acgcaacgcc
900
gacgggcccgc ggcttaaagc gccgactgag aacatcatcg ttcaaggatg tcgcatgaaa
960
gacggccacg gtggaatcac ggtcggcagc gagatctcgg gcggcggtcg aaacctgttt
1020
gccgagaatt gccggctcga cagtccaaac ctcgatcacg ccctgcgcgt gaagaacaat
1080
gccatgcgcg gcggattact cgagaacttc cacttcgta acatcgaagt cgggcagggtg
1140
gcccattgcc tgattacgat cgacttcaac tacgaagagg gcgcgaaagg gtcgttcacg
1200
ccggtcgttc gcgattacac ggtcgatcgt ttgcgcagca cgaagagcaa gcacgcactc
1260
gacgtccagg gtctgcccgg cgcgccggtc atcaacctgc gattgacaaa ctgcacattc
1320
aacgatgtgc agcaaccgaa cattctcaag aacgtcgaac aatcaacctt tgagaacgtc
1380
acgattaacg gaaagacgat cacacaaaca ggatccatct cagaaagagc ggccacgaca
1440
gcaatgaccg cgctttggcg cgacgcgtcg aggaaagaaa acggttatcc cggaagtgg
1500
acctatgatc atgggctggt cctgaaagga atcgagcgcg tttggaacaa taccggcgat
1560
aagaagtatc tgaagttcat ccaggacagc atggaccact tcgtcaacga cgacggctcc
1620
attcgcacct acacgatcga cgagtacaac atcgatcacg ttcttcccg acgaaacctc
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1740

gaacaa
1746

<210> 80
<211> 582
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN
<222> (81)...(458)
<223> Catalytic domain

<400> 80

Met	Thr	Thr	Arg	Arg	Glu	Phe	Ile	Lys	Gly	Phe	Leu	Leu	Thr	Gly	Ala
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Ala	Val	Ala	Val	Ala	Pro	Arg	Leu	Ile	Ala	Phe	Gly	Ala	Glu	Ala	Ser
			20					25					30		
Pro	Trp	Glu	Thr	Met	Met	Pro	Ser	Ile	Leu	Ala	Arg	Ile	Thr	Pro	Pro
		35					40					45			
Arg	Phe	Pro	Lys	Arg	Thr	Phe	Tyr	Leu	Asn	Arg	Phe	Gly	Ala	Lys	Gly
	50					55					60				
Asp	Gly	Val	Thr	Asp	Cys	Thr	Ala	Ala	Phe	His	Arg	Ala	Ile	Asp	Glu
65					70					75				80	
Cys	Thr	Lys	Ala	Gly	Gly	Gly	Lys	Val	Val	Val	Pro	Ala	Gly	Thr	Tyr
				85					90					95	
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Val	Ser
			100					105					110		
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asp	Pro	Lys	His	Tyr	Leu	Pro
		115					120					125			
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
	130					135					140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Arg	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
145					150					155				160	
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Ser	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
			165						170					175	
Arg	Pro	Gln	Tyr	Gly	Trp	Asn	Glu	Gly	Met	Lys	Gln	Gln	Arg	Pro	Asp
			180					185					190		
Arg	Asn	Ala	Leu	Phe	Thr	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Arg	Glu
		195					200					205			
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
	210					215					220				
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Gln	Gly	Val	Thr	Ile	Arg	Asn	Ser
225					230					235				240	
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Thr	Ile	His
				245					250					255	
Asp	Val	His	Ile	Asp	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
			260					265					270		
Glu	Ser	Cys	Ser	Asp	Val	Leu	Ile	Lys	Asp	Ser	Tyr	Phe	Asp	Thr	Gly
		275					280					285			
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
	290					295					300				
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Gln	Gly	Cys	Arg	Met	Lys
305					310					315				320	
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
			325						330					335	

Arg Asn Leu Phe Ala Glu Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
 340 345 350
 His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
 355 360 365
 Asn Phe His Phe Arg Asn Ile Glu Val Gly Gln Val Ala His Ala Val
 370 375 380
 Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
 385 390 395 400
 Pro Val Val Arg Asp Tyr Thr Val Asp Arg Leu Arg Ser Thr Lys Ser
 405 410 415
 Lys His Ala Leu Asp Val Gln Gly Leu Pro Gly Ala Pro Val Ile Asn
 420 425 430
 Leu Arg Leu Thr Asn Cys Thr Phe Asn Asp Val Gln Gln Pro Asn Ile
 435 440 445
 Leu Lys Asn Val Glu Gln Ser Thr Phe Glu Asn Val Thr Ile Asn Gly
 450 455 460
 Lys Thr Ile Thr Gln Thr Gly Ser Ile Ser Glu Arg Ala Ala Thr Thr
 465 470 475 480
 Ala Met Thr Ala Leu Trp Arg Asp Ala Ser Arg Lys Glu Asn Gly Tyr
 485 490 495
 Pro Ala Lys Trp Thr Tyr Asp His Gly Leu Val Leu Lys Gly Ile Glu
 500 505 510
 Arg Val Trp Asn Asn Thr Gly Asp Lys Lys Tyr Leu Lys Phe Ile Gln
 515 520 525
 Asp Ser Met Asp His Phe Val Asn Asp Asp Gly Ser Ile Arg Thr Tyr
 530 535 540
 Thr Ile Asp Glu Tyr Asn Ile Asp His Val Leu Pro Gly Arg Asn Leu
 545 550 555 560
 Leu Phe Leu Tyr Lys Thr Thr Gly Gln Glu Lys Tyr Arg Lys Ala Ala
 565 570 575
 Ala Phe Leu Arg Glu Gln
 580

<210> 81
 <211> 1065
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 81
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 120
 ctgctgcaga ccgcctccgg tggctggtcc aagcactacc gcgggaagaa ggtcgactac
 180
 acgcgcaatt acgacaccgc cgagcgcgcc gcgctgcgcg cgcccggccg gcatgacgac
 240
 gcgacgatcg acaacaaggc cacgaccagc gagatcgctt acctggtgca ggcacatgcc
 300
 aggacgggca acccggcgta cctcgacggt gcccgccgcg gggtcgaata cctgctgcgc
 360
 gcgcagtacc cgaatggtgg ctggccgcag ttctaccccg accactcgtc ctaccggcac
 420
 cagatcacgc tcaacgacga cgcgatggtg catgccatca ccgtgctgca ggacatcgcc
 480
 gccggccgcg acggcatgca ggcgttgacg cccgagttcg gcgtccgcgc cgccgcccgc
 540
 gcgcagcgcg gcatcggaac cctgctcgag ttgcaggtgc ggatcgacgg cgagccgacc

600
 atctgggccc cgagtagcga cgagcatagc ctgcagccgg ccaaggcccc cgcctatgaa
 660
 ctgccctcgc tggccgtggc cgaatcggtc ggcgtggtgc gcctgctgat gcgccagccc
 720
 aggccggatg cccggaccgt cgccgcgac gaatcggcgg cccgctggct ggaggcgcac
 780
 cgcctgcatg acctggcgct cgaacgcgtc gacgcaccgg ccgaggaaac gggcaaggac
 840
 gtgcgggtcg tgaccgggcc cggcgccctc ctgtggggcg gcttctacga cctggatgga
 900
 cagcagcctc tgttcgtcga ccgcgacagc aagccccgtcc cgttcgccag cctgcccac
 960
 gagcgccgca ccggctatgc ctggtacggc acctggccgg agaagctgct ggcgcaggaa
 1020
 ctcccgcgt ggcgcgaggt ccatgccgcc ggcgccgcgc cctga
 1065

<210> 82
 <211> 354
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(30)

<221> DOMAIN
 <222> (31)...(354)
 <223> Catalytic domain

<400> 82
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 Thr Leu Pro Val Ala Cys Ala Gly Ala Ala Val Ser Ala Ala Ala Thr
 20 25 30
 Asp Pro Val Ala Glu Asn Met Leu Leu Gln Thr Ala Ser Gly Gly
 35 40 45
 Trp Ser Lys His Tyr Arg Gly Lys Lys Val Asp Tyr Thr Arg Asn Tyr
 50 55 60
 Asp Thr Ala Glu Arg Ala Ala Leu Arg Ala Pro Gly Arg His Asp Asp
 65 70 75 80
 Ala Thr Ile Asp Asn Lys Ala Thr Thr Ser Glu Ile Ala Tyr Leu Val
 85 90 95
 Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
 100 105 110
 Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
 115 120 125
 Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
 130 135 140
 Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
 145 150 155 160
 Ala Gly Arg Asp Gly Met Gln Ala Leu Thr Pro Glu Phe Gly Val Arg
 165 170 175
 Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
 180 185 190
 Val Arg Ile Asp Gly Glu Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
 195 200 205
 His Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu

210	215	220
Ala Val Ala Glu Ser Val Gly Val Val Arg Leu	Leu Met Arg Gln Pro	
225	230	235
Arg Pro Asp Ala Arg Thr Val Ala Ala Ile Glu	Ser Ala Ala Arg Trp	240
	245	250
Leu Glu Ala His Arg Leu His Asp Leu Ala Leu	Glu Arg Val Asp Ala	255
	260	265
Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val	Val Thr Arg Pro Gly	270
	275	280
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Asp	Gly Gln Gln Pro Leu	285
	290	295
Phe Val Asp Arg Asp Ser Lys Pro Val Pro Phe	Ala Ser Leu Pro Asn	300
305	310	315
Glu Arg Arg Thr Gly Tyr Ala Trp Tyr Gly Thr	Trp Pro Glu Lys Leu	320
	325	330
Leu Ala Gln Glu Leu Pro Arg Trp Arg Glu Val	His Ala Ala Gly Ala	335
	340	345
		350
Ala Pro		

<210> .83
 <211> 3618
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 83
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 60
 caggtaacct acaatctaaa acgcagtacc acgaaggagg gtccttatca gaccattgct
 120
 gaaaaaatgg cagaaaccga cttccgggat acaggggttag agaatggcca gaagtattac
 180
 tatgttgtat ctgccgaaac gagtagcggg gagagtgcag attcacaagc tataacggct
 240
 gtgcctgtag cgccattgca agctccgacc ggcctttcag caagtcattg caatggcggg
 300
 gtaaccattc attgggaatc cgtcaatggt gccgagtcctt accaagtcctt gcgcagtaaa
 360
 caaaagggca tcggctatga agtcatcaaa aacgggtgtaa cggaaccag ttatacagat
 420
 accgggattc ccgatggcga gaagtactat tatgtcgtat ccgccaagaa cgatacagct
 480
 gaaagtgcaa attcccaacc gattaacggg gctgctgtat cgacgagtgg tgtaccagcc
 540
 attccaaacg gtatgaacgc tactgccggg gatggcagag ctgccttaac ctggtccgct
 600
 gtatccggcg cagattccta tagcatcaag cgcggtgagt ttaacagtgg tcaatatgag
 660
 gtcattgcta aaaatataca ctctaccggg tatcaagata taggccttac aaacgggtgag
 720
 acctatgatt atgtgatttc cgctgtcaat gagcaagggg aaagtttagg ctccgaaccc
 780
 atcgccgtta ctctgcgaa agtaacgggt gtagcgaaaag aaggcggaga ctttaaaacg
 840
 attcaagaag ccattgatgc tgcacctgat aacagtacga aacggcatgt tatttttata
 900
 aaaaatggtc aatatcgtga aaagcttacg atccctaaga gcaaaaacaa tctgagtttt
 960

gtaggggaaa gtaaggaagg gaccgtgctt gtttttaatg ataatgcaaa tacgcctggg
 1020
 ccagacggca aaccattagg cacttccaat agttcaagta tctttatcta tgccaatgat
 1080
 tttattgccc aaaatttaac catccagaac gactctggtc aaggaacagg tcaagcagtt
 1140
 gccgcttatg taagggccga tcgtctctac tttgaaaacg tgcagttttt aggataccag
 1200
 gatacattat atgcccatac gggaagacag tattataaaa actgctacgt agaaggggat
 1260
 gtggatttca tttttggcgg agccacagcc ttgtttgata cctgtcacct tcatagcaag
 1320
 cgtacaggca gtaagttaac cgcagctagt accgatcaag tcacaccgta tgggtatggt
 1380
 ttttttagatt caaaaatcac ctcagatgaa ggcgtgacca atgtgcatct cgggcgacct
 1440
 tggcgtcctt attcagctgt cacctatatac aacaccgaaa tggatgcatc gattgttcct
 1500
 gacggatggg ataactgggg gaaagttgaa aacgagaaaa cagccagata ttcagaatac
 1560
 aataacatgg ggccaggggc agaccgaaa aagcgggatc catggaccac acaattaacg
 1620
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 1680
 cctgagagaa tcgggattat cccattatca ccactgtcag caccgattat ttcacttgat
 1740
 caacgagatt ccattgtcaa tacaccaagc tttacaatta caggtcaagt ggataaagaa
 1800
 gcagccgttt ctgtcaatgg gaaggaaatt tccttacaaa aggatggcag cttcagcacg
 1860
 acggtgggtgc tgaatgacgg tttgaacact attacagtgg gagctgtaga tgcagcaggg
 1920
 aatcaggcta ttctgtcagt gttaaaaatt gtttatgatac atgagaaaacc tgtcgtatcc
 1980
 atcgatgatac ttaaaggaga aaaaaacggg aatcactaca atgtaatcta caatccgctg
 2040
 ccgattacag ggaagctgaa cgaagcagga acagtatatg tgaatggatga gaaagtaaat
 2100
 gtatcggaag agttgacgtt tagtacaaaa gtcatttttaa agccgggggtt aaataacatt
 2160
 acgattaccg ctgttgatca ggcagggaat gaagccgaat ctatcactat caatgtgggt
 2220
 ccaaaagggg atgctgttcc agacggtccc gtcaagatta tcaaaagtga aacaacaaat
 2280
 gcaaataccg ttgaggttac ttttaatagc aagctagaaa aatttgattc tagtgatatt
 2340
 gcattgcaaa cggctacgaa cgtttgggca gctctcaatc ctggtttgaa acaattgatg
 2400
 acagtggaaa gcattaccac aaaagtgaat aaggataacc aaaccgtagc ggtgatcaaa
 2460
 acgaaggaag cctttcaaga agatggaacc attacgtccc caaaagtga agatccggtt
 2520
 catattcaat atttgaatgc cgattattat accggggatc gtacgcagga cattaagcat
 2580
 gcggatgccc tcttaacctg gcagatggat catggcggct ggtttaaaaa ctgggtggaa
 2640
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 2700
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 2760
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2820
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 2880
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 2940
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 3000
 cagattgatg atgcattggg ccgtgggctg gattatatgt taaaatcgca aattaaggta
 3060
 gacggtgaag taaccgcatg gtgtgctcag catgaccctg tgacgtatga accgaaagg
 3120
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 3180
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 3240
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 3360
 cgcccattt tctcaggaag agacggtgtc attaaacaca acatcttaga gattgaaaaa
 3420
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 3480
 aacacaactg gctactacga aaacagagta tacgtagaag tcgttgggga tcagtctaaa
 3540
 aacgccgctg gcgaatcttt ggaaatagga aacttatata gaatagaggc ctcggcttcc
 3600
 ggttctacaa gcaagtaa
 3618

<210> 84
 <211> 1205
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (268)...(556)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (782)...(1164)
 <223> Catalytic domain

<400> 84
 Met Thr Ala Leu Ser Arg Asn Ser Gln Val Asp Val Ser Trp Glu Pro
 1 5 10 15
 Ser Ser Ala Gln Gln Val Thr Tyr Asn Leu Lys Arg Ser Thr Thr Lys
 20 25 30
 Glu Gly Pro Tyr Gln Thr Ile Ala Glu Lys Met Ala Glu Thr Asp Phe
 35 40 45
 Arg Asp Thr Gly Leu Glu Asn Gly Gln Lys Tyr Tyr Tyr Val Val Ser
 50 55 60
 Ala Glu Thr Ser Ser Gly Glu Ser Ala Asp Ser Gln Ala Ile Thr Ala
 65 70 75 80
 Val Pro Val Ala Pro Leu Gln Ala Pro Thr Gly Leu Ser Ala Ser His
 85 90 95
 Gly Asn Gly Gly Val Thr Ile His Trp Glu Ser Val Asn Gly Ala Glu
 100 105 110

Ser	Tyr	Gln	Val	Leu	Arg	Ser	Lys	Gln	Lys	Gly	Ile	Gly	Tyr	Glu	Val
		115					120					125			
Ile	Lys	Asn	Gly	Val	Thr	Glu	Thr	Ser	Tyr	Thr	Asp	Thr	Gly	Ile	Pro
	130					135					140				
Asp	Gly	Glu	Lys	Tyr	Tyr	Tyr	Val	Val	Ser	Ala	Lys	Asn	Asp	Thr	Ala
145					150					155					160
Glu	Ser	Ala	Asn	Ser	Gln	Pro	Ile	Asn	Gly	Ala	Ala	Val	Ser	Thr	Ser
			165						170					175	
Gly	Val	Pro	Ala	Ile	Pro	Asn	Gly	Met	Asn	Ala	Thr	Ala	Gly	Asp	Gly
			180					185					190		
Arg	Ala	Ala	Leu	Thr	Trp	Ser	Ala	Val	Ser	Gly	Ala	Asp	Ser	Tyr	Ser
	195					200						205			
Ile	Lys	Arg	Gly	Glu	Phe	Asn	Ser	Gly	Gln	Tyr	Glu	Val	Ile	Ala	Lys
	210					215					220				
Asn	Ile	His	Ser	Thr	Gly	Tyr	Gln	Asp	Ile	Gly	Leu	Thr	Asn	Gly	Asp
225					230					235					240
Thr	Tyr	Asp	Tyr	Val	Ile	Ser	Ala	Val	Asn	Glu	Gln	Gly	Glu	Ser	Leu
				245					250					255	
Gly	Ser	Glu	Pro	Ile	Ala	Val	Thr	Pro	Ala	Lys	Val	Thr	Val	Val	Ala
			260					265					270		
Lys	Glu	Gly	Gly	Asp	Phe	Lys	Thr	Ile	Gln	Glu	Ala	Ile	Asp	Ala	Ala
	275						280					285			
Pro	Asp	Asn	Ser	Thr	Lys	Arg	His	Val	Ile	Phe	Ile	Lys	Asn	Gly	Gln
	290					295					300				
Tyr	Arg	Glu	Lys	Leu	Thr	Ile	Pro	Lys	Ser	Lys	Thr	Asn	Leu	Ser	Phe
305					310					315					320
Val	Gly	Glu	Ser	Lys	Glu	Gly	Thr	Val	Leu	Val	Phe	Asn	Asp	Asn	Ala
				325					330					335	
Asn	Thr	Pro	Gly	Pro	Asp	Gly	Lys	Pro	Leu	Gly	Thr	Ser	Asn	Ser	Ser
			340					345					350		
Ser	Ile	Phe	Ile	Tyr	Ala	Asn	Asp	Phe	Ile	Ala	Gln	Asn	Leu	Thr	Ile
	355						360					365			
Gln	Asn	Asp	Ser	Gly	Gln	Gly	Thr	Gly	Gln	Ala	Val	Ala	Ala	Tyr	Val
	370					375					380				
Arg	Ala	Asp	Arg	Leu	Tyr	Phe	Glu	Asn	Val	Gln	Phe	Leu	Gly	Tyr	Gln
385					390					395					400
Asp	Thr	Leu	Tyr	Ala	His	Thr	Gly	Arg	Gln	Tyr	Tyr	Lys	Asn	Cys	Tyr
				405					410					415	
Val	Glu	Gly	Asp	Val	Asp	Phe	Ile	Phe	Gly	Gly	Ala	Thr	Ala	Leu	Phe
			420					425					430		
Asp	Thr	Cys	His	Leu	His	Ser	Lys	Arg	Thr	Gly	Ser	Lys	Leu	Thr	Ala
	435						440					445			
Ala	Ser	Thr	Asp	Gln	Val	Thr	Pro	Tyr	Gly	Tyr	Val	Phe	Leu	Asp	Ser
	450					455					460				
Lys	Ile	Thr	Ser	Asp	Glu	Gly	Val	Thr	Asn	Val	His	Leu	Gly	Arg	Pro
465					470					475					480
Trp	Arg	Pro	Tyr	Ser	Ala	Val	Thr	Tyr	Ile	Asn	Thr	Glu	Met	Asp	Ala
				485					490					495	
Ser	Ile	Val	Pro	Asp	Gly	Trp	Asp	Asn	Trp	Gly	Lys	Val	Glu	Asn	Glu
			500					505					510		
Lys	Thr	Ala	Arg	Tyr	Ser	Glu	Tyr	Asn	Asn	Met	Gly	Pro	Gly	Ala	Asp
	515						520					525			
Pro	Lys	Lys	Arg	Asp	Pro	Trp	Thr	Thr	Gln	Leu	Thr	Pro	Glu	Glu	Ala
	530					535						540			
Asn	Gln	Tyr	Thr	Val	Gln	Asn	Val	Met	Lys	Gly	Ser	Asp	Gly	Trp	Asp
545					550					555					560
Pro	Glu	Arg	Ile	Gly	Ile	Ile	Pro	Leu	Ser	Pro	Leu	Ser	Ala	Pro	Ile
				565					570					575	
Ile	Ser	Leu	Asp	Gln	Arg	Asp	Ser	Ile	Val	Asn	Thr	Pro	Ser	Phe	Thr
			580					585					590		
Ile	Thr	Gly	Gln	Val	Asp	Lys	Glu	Ala	Ala	Val	Ser	Val	Asn	Gly	Lys

		595					600					605					
Glu	Ile	Ser	Leu	Gln	Lys	Asp	Gly	Ser	Phe	Ser	Thr	Thr	Val	Val	Leu		
	610					615					620						
Asn	Asp	Gly	Leu	Asn	Thr	Ile	Thr	Val	Gly	Ala	Val	Asp	Ala	Ala	Gly		
625					630					635					640		
Asn	Gln	Ala	Ile	Pro	Ala	Val	Leu	Lys	Ile	Val	Tyr	Asp	His	Glu	Lys		
				645					650					655			
Pro	Val	Val	Ser	Ile	Asp	Asp	Leu	Lys	Gly	Glu	Lys	Asn	Gly	Asn	His		
			660				665					670					
Tyr	Asn	Val	Ile	Tyr	Asn	Pro	Leu	Pro	Ile	Thr	Gly	Lys	Leu	Asn	Glu		
	675						680					685					
Ala	Gly	Thr	Val	Met	Val	Asn	Gly	Glu	Lys	Val	Asn	Val	Ser	Glu	Lys		
	690					695					700						
Leu	Thr	Phe	Ser	Thr	Lys	Val	Ile	Leu	Lys	Pro	Gly	Leu	Asn	Asn	Ile		
705					710					715					720		
Thr	Ile	Thr	Ala	Val	Asp	Gln	Ala	Gly	Asn	Glu	Ala	Glu	Ser	Ile	Thr		
				725				730						735			
Ile	Asn	Val	Val	Pro	Lys	Gly	Asn	Ala	Val	Pro	Asp	Gly	Pro	Val	Lys		
			740				745					750					
Ile	Ile	Lys	Ser	Glu	Thr	Thr	Asn	Ala	Asn	Thr	Val	Glu	Val	Thr	Phe		
	755					760					765						
Asn	Ser	Lys	Leu	Glu	Lys	Phe	Asp	Ser	Ser	Asp	Ile	Ala	Leu	Gln	Thr		
	770					775					780						
Ala	Thr	Asn	Val	Trp	Ala	Ala	Leu	Asn	Pro	Gly	Leu	Lys	Gln	Leu	Met		
785					790					795					800		
Thr	Val	Glu	Ser	Ile	Thr	Thr	Lys	Val	Asn	Lys	Asp	Asn	Gln	Thr	Val		
				805					810					815			
Ala	Val	Ile	Lys	Thr	Lys	Glu	Ala	Phe	Gln	Glu	Asp	Gly	Thr	Ile	Thr		
			820					825					830				
Leu	Pro	Lys	Val	Glu	Asp	Pro	Phe	His	Ile	Gln	Tyr	Leu	Asn	Ala	Asp		
	835						840					845					
Tyr	Tyr	Thr	Gly	Asp	Arg	Thr	Gln	Asp	Ile	Lys	His	Ala	Asp	Ala	Leu		
	850					855					860						
Leu	Thr	Trp	Gln	Met	Asp	His	Gly	Gly	Trp	Phe	Lys	Asn	Trp	Val	Glu		
865					870					875					880		
Lys	Tyr	Lys	Arg	Pro	Trp	Asp	Gly	Lys	Glu	Pro	Lys	Ser	Glu	Trp	Tyr		
			885						890					895			
Ser	Thr	Asn	His	Gly	Glu	Leu	Gly	Thr	Ile	Asp	Asn	Asp	Ala	Thr	Thr		
			900					905					910				
Asn	Glu	Ile	Leu	Phe	Leu	Ala	Leu	Met	Tyr	Lys	Glu	Thr	Gly	Asp	Ala		
	915						920					925					
Arg	Tyr	Lys	Asp	Ser	Val	Leu	Lys	Gly	Ile	Asp	Phe	Leu	Leu	Glu	Met		
	930					935					940						
Gln	Val	Asp	Ser	Gly	Gly	Trp	Pro	Gln	Val	Tyr	Pro	Ala	Arg	Ser	Gly		
945					950					955					960		
Tyr	Ser	Asp	Tyr	Val	Thr	Phe	Asn	Asp	Asn	Ala	Met	Val	Arg	Val	Met		
			965						970					975			
Ser	Val	Leu	Thr	Met	Val	Lys	Glu	Lys	Tyr	Pro	Phe	Asn	Ser	Asn			
			980					985					990				
Leu	Gly	Asp	Glu	Gln	Leu	Ser	Glu	Gln	Ile	Asp	Asp	Ala	Leu	Gly	Arg		
	995						1000					1005					
Gly	Leu	Asp	Tyr	Met	Leu	Lys	Ser	Gln	Ile	Lys	Val	Asp	Gly	Glu	Val		
	1010					1015					1020						
Thr	Ala	Trp	Cys	Ala	Gln	His	Asp	Pro	Val	Thr	Tyr	Glu	Pro	Lys	Gly		
1025					1030					1035					1040		
Ala	Arg	Ala	Tyr	Glu	His	Pro	Ser	Ile	Ser	Gly	Ser	Glu	Ser	Val	Gly		
			1045						1050					1055			
Ile	Val	Gln	Tyr	Leu	Met	Ser	Leu	Pro	Asn	Pro	Ser	Thr	Glu	Val	Gln		
			1060					1065				1070					
Ala	Ala	Ile	His	Gly	Ala	Leu	Asn	Trp	Phe	Glu	Glu	Ala	Lys	Leu	Ala		
	1075						1080					1085					

Gly Thr Lys Tyr Val Ser Gly Asp Pro Asn Gly Gln Tyr Phe Tyr Pro
 1090 1095 1100
 Asp Ala Asn Ser Asn Thr Trp Tyr Arg Phe Tyr Glu Ile Gly Thr Asn
 1105 1110 1115 1120
 Arg Pro Ile Phe Ser Gly Arg Asp Gly Val Ile Lys His Asn Ile Leu
 1125 1130 1135
 Glu Ile Glu Lys Glu Arg Arg Asp Gly Tyr Arg Trp Ala Gly Glu Trp
 1140 1145 1150
 Pro Gln Lys Leu Leu Asn Ile Ala Asn Thr Thr Gly Tyr Tyr Glu Asn
 1155 1160 1165
 Arg Val Tyr Val Glu Val Val Gly Asp Gln Ser Lys Asn Ala Ala Gly
 1170 1175 1180
 Glu Ser Leu Glu Ile Gly Asn Leu Tyr Arg Ile Glu Ala Ser Ala Ser
 1185 1190 1195 1200
 Gly Ser Thr Ser Lys
 1205

<210> 85
 <211> 1152
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 85
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 ggtgttgagg caaagctgtt tcagcgcgag cggttcttca gcctcgtgc ggagcacact
 120
 tctaagaaaa atgatacagga agtcggcgcg atcgcgtgga aagatgcaca tggaaagccg
 180
 gatgagtggg atgcgagtgt tgaggcactg cggatggccg ataacgtcgt tctctatcaa
 240
 cgcgactcag gtggttgagg caagaacatc gacatggcga aggcactcaa cgatcgtgag
 300
 caggctgcga tcctccgcca gaagaaaaag aacgactcca cgatcgacaa tgggtgcgact
 360
 cacacacagt taccctttct ggcgcgcgtc tatacagcac agcgtcagga gcgacatcgc
 420
 gagtcgtttt tcaaaggatt ggattactta ctgaatgcgc agtatccaaa tggaggctgg
 480
 ccgcagtttt atccgaaccc gacgggctat cacaagcaca ttacttacia cgacggtgcg
 540
 atgattggtg tgatgaagggt gctgcgcgat atcgtctcgg cgaagccttt gtacgctttt
 600
 gtcgacgaag ctcggcgcgcg gaaggcgacg agtgcagttg aaaaagggat cgagtgcatt
 660
 ttgaaaacgc aggtggtggt agatggcgt cgactgtgt ggagtgcgca acatgatgaa
 720
 gtaacgtagg cgccagctcc tgcgcgaacc ttcgagttaa cttcgttgag cggcggtgag
 780
 agcgtagata tcgttcgatt ttaaatgtcg atcaaggatc cgtcgcctaa agtagttgat
 840
 gcggttgaat cggcggttaa gtggtttgag caatcggagt taaaaggcgt gaagtgggtt
 900
 aagaaggcgg acgcttctaa acctggcggg tttgattgcy tcgtagttaa ggatccggag
 960
 agctcggttt gggcgcgctt ttatgagatt ggcacgaacc ggccgatctt ttccgggcgc
 1020
 gatggagtgg tcaaatacga cgtggcgag atcgaacacg agcggcgac gaattatgag

1080
 tggtagcttg atgaagcagc caagctgctg aagaaagagt atccggcctg gcggaaaaga
 1140
 acatctctgt ga
 1152

<210> 86
 <211> 383
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(383)
 <223> Catalytic domain

<400> 86
 Met Ser Val Gly Pro Gly Ala Asn Pro Lys Ala Arg Val Pro Trp Ser
 1 5 10 15
 Lys Gln Leu Ser Gly Val Glu Ala Lys Leu Phe Gln Arg Glu Arg Phe
 20 25 30
 Phe Ser Leu Ala Ala Glu His Thr Ser Lys Lys Asn Asp Gln Glu Val
 35 40 45
 Gly Ala Ile Ala Trp Lys Asp Ala His Gly Lys Pro Asp Glu Trp Tyr
 50 55 60
 Ala Ser Val Glu Ala Leu Arg Met Ala Asp Asn Val Val Leu Tyr Gln
 65 70 75 80
 Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Lys Ala Leu
 85 90 95
 Asn Asp Arg Glu Gln Ala Ala Ile Leu Arg Gln Lys Lys Lys Asn Asp
 100 105 110
 Ser Thr Ile Asp Asn Gly Ala Thr His Thr Gln Leu Ser Phe Leu Ala
 115 120 125
 Arg Val Tyr Thr Ala Gln Arg Gln Glu Arg His Arg Glu Ser Phe Phe
 130 135 140
 Lys Gly Leu Asp Tyr Leu Leu Asn Ala Gln Tyr Pro Asn Gly Gly Trp
 145 150 155 160
 Pro Gln Phe Tyr Pro Asn Pro Thr Gly Tyr His Lys His Ile Thr Tyr
 165 170 175
 Asn Asp Gly Ala Met Ile Gly Val Met Lys Val Leu Arg Asp Ile Ala
 180 185 190
 Ala Ala Lys Pro Leu Tyr Ala Phe Val Asp Glu Ala Arg Arg Ala Lys
 195 200 205
 Ala Thr Ser Ala Val Glu Lys Gly Ile Glu Cys Ile Leu Lys Thr Gln
 210 215 220
 Val Val Val Asp Gly Arg Arg Thr Val Trp Ser Ala Gln His Asp Glu
 225 230 235 240
 Val Thr Leu Ala Pro Ala Pro Ala Arg Thr Phe Glu Leu Thr Ser Leu
 245 250 255
 Ser Gly Gly Glu Ser Val Asp Ile Val Arg Phe Leu Met Ser Ile Lys
 260 265 270
 Asp Pro Ser Pro Lys Val Val Asp Ala Val Glu Ser Ala Val Lys Trp
 275 280 285
 Phe Glu Gln Ser Glu Leu Lys Gly Val Lys Trp Val Lys Lys Ala Asp
 290 295 300
 Ala Ser Lys Pro Gly Gly Phe Asp Cys Val Val Val Lys Asp Pro Glu
 305 310 315 320
 Ser Ser Val Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile
 325 330 335

Phe	Ser	Gly	Arg	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Ala	Gln	Ile	Glu
			340					345					350		
His	Glu	Arg	Arg	Thr	Asn	Tyr	Glu	Trp	Tyr	Val	Asp	Glu	Ala	Ala	Lys
		355					360					365			
Leu	Leu	Lys	Lys	Glu	Tyr	Pro	Ala	Trp	Arg	Lys	Arg	Thr	Ser	Leu	
	370					375					380				

<210> 87
 <211> 1698
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 87
 atgtctacta caaaatgttt taacacagcc ccagggtttta ccctgaaagc agtcgcagca
 60
 gcagtgccga tgtttgcagg ttcttcagta ttccgcagcg ctacaggtgg tttttccacg
 120
 actgatggcg gtgcggcaag cggctcgcaa tccttcacgg cggccaacct tgaccagctc
 180
 aacaccattg ttgccaatgc gaagagtggc gggtaccggg ttgtgattac ctataccggg
 240
 aatgaagaca gcttgattaa ccagatgatc aaagaccaca ccgtggattc ttcaggcaac
 300
 tgcccgaacc cacgctggag tgaaacctac cgcaaggtag aaattaagga gatgaccaa
 360
 ggtgtcacca tcatcgggtc caatggttct tcggcaaact tcggtattgt ggtgaacaag
 420
 tccagcaatg tgattatccg caacatgaaa atcgggtgcgc tggccgggtc cagcaacgac
 480
 gcggatatga ttctgtatcga tagcggcact aacgtatggg ttgaccacaa cgaattgttc
 540
 gcggtgaaca acgaatgtaa aggttcaccg gatggcgatt tgaccttcga aagcgccatc
 600
 gacatcaaga aagattcaca caacatcacc gtgtcttaca acctgattcg cgacagcaaa
 660
 aaagtgggccc ttgatgggtc cagcagcagc gatatcgccg gtggccgcga gatcactttc
 720
 caccacaaca tttacaaaaa cgtgaatgca cgcttgccgt tgcaacgcgg tggctggacg
 780
 cacatgtata acaacctgta cgacggcatt accggttccg gtatcaacgt acgtcaggcc
 840
 gggttatgctg tgattgaaag caactgggtc caaaatgcgg ttaaccgggt gacttgccgt
 900
 tacgacagca gcaactgcgg tttctgggat ctgcgcaata acaacgtgaa gtcgccagca
 960
 gatttcgcga cctataacat cacctggacc agcggcggca ctattgatgc aaccaactgg
 1020
 acgaccaccg ctccgttccc gatcagcatt ccttacagct actcgccggg gtctccacag
 1080
 tgcgtgaagg acaagtggc cagcgttgcg ggtgtgggta aaaacgggtg agttctgaac
 1140
 tcatcagtgt gtggtggaag cagctctgtt ccatcatcaa gctcagtcgc tactacttcc
 1200
 aaatcatcca gtcggtagc aaccagcaag tccagctccg tcgctacgac gtccagtaag
 1260
 tcatccagct cggtagtgcc atcatcatca agctcaagtt cagtgggtta taacggcagc
 1320
 atcgcggtta ccgccactgc taccggcaat agcattgtcc tgagctggtc gccgaacaac

1380
ctgacactgg gcacccagga ggtgtatcgc gataccgatt cagaccaag tggccgtgtg
1440
cgtattgctg ccctgagttc cagcactcgc atgtacaccg atgccactgc atcggcgggc
1500
caaacgttct actactggat caaaaacacc accaacggtg taaccaccaa ttccaatgcg
1560
gcttcggcgg caattggcga tgcagctcgc gccattcgcg catgcgccagg aaaccgagga
1620
agtggcgctc gcaccagtcg cgcagtttcg actgggtcaa atcctcgtgg gcctgcccgt
1680
agccatccca gagcttga
1698

<210> 88
<211> 565
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(375)
<223> Catalytic domain

<400> 88
Met Ser Thr Thr Lys Cys Phe Asn Thr Ala Pro Gly Phe Thr Leu Lys
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Ala Val Ala Ala Val Ala Met Phe Ala Gly Ser Ser Val Phe Ala
20 25 30
Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Ala Ala Ser Gly
35 40 45
Ser Gln Ser Phe Thr Ala Ala Asn Leu Asp Gln Leu Asn Thr Ile Val
50 55 60
Ala Asn Ala Lys Ser Gly Gly Tyr Pro Val Val Ile Thr Tyr Thr Gly
65 70 75 80
Asn Glu Asp Ser Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asp
85 90 95
Ser Ser Gly Asn Cys Pro Asn Pro Arg Trp Ser Glu Thr Tyr Arg Lys
100 105 110
Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Ile Gly Ala Asn
115 120 125
Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser Ser Asn Val
130 135 140
Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp
145 150 155 160
Ala Asp Met Ile Arg Ile Asp Ser Gly Thr Asn Val Trp Val Asp His
165 170 175
Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly
180 185 190
Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Asp Ser His Asn
195 200 205
Ile Thr Val Ser Tyr Asn Leu Ile Arg Asp Ser Lys Lys Val Gly Leu
210 215 220
Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Glu Ile Thr Phe
225 230 235 240
His His Asn Ile Tyr Lys Asn Val Asn Ala Arg Leu Pro Leu Gln Arg

				245					250					255			
Gly	Gly	Trp	Thr	His	Met	Tyr	Asn	Asn	Leu	Tyr	Asp	Gly	Ile	Thr	Gly		
			260					265					270				
Ser	Gly	Ile	Asn	Val	Arg	Gln	Ala	Gly	Tyr	Ala	Leu	Ile	Glu	Ser	Asn		
		275					280					285					
Trp	Phe	Gln	Asn	Ala	Val	Asn	Pro	Val	Thr	Cys	Arg	Tyr	Asp	Ser	Ser		
	290					295					300						
Asn	Cys	Gly	Phe	Trp	Asp	Leu	Arg	Asn	Asn	Asn	Val	Lys	Ser	Pro	Ala		
305					310				315						320		
Asp	Phe	Ala	Thr	Tyr	Asn	Ile	Thr	Trp	Thr	Ser	Gly	Gly	Thr	Ile	Asp		
			325					330						335			
Ala	Thr	Asn	Trp	Thr	Thr	Thr	Ala	Pro	Phe	Pro	Ile	Ser	Ile	Pro	Tyr		
		340						345					350				
Ser	Tyr	Ser	Pro	Val	Ser	Pro	Gln	Cys	Val	Lys	Asp	Lys	Leu	Ala	Ser		
		355					360				365						
Val	Ala	Gly	Val	Gly	Lys	Asn	Gly	Ala	Val	Leu	Asn	Ser	Ser	Val	Cys		
	370					375					380						
Gly	Gly	Ser	Ser	Ser	Val	Pro	Ser	Ser	Ser	Ser	Val	Ala	Thr	Thr	Ser		
385					390				395						400		
Lys	Ser	Ser	Ser	Ser	Val	Ala	Thr	Ser	Lys	Ser	Ser	Ser	Val	Ala	Thr		
			405						410					415			
Thr	Ser	Ser	Lys	Ser	Ser	Ser	Ser	Val	Val	Pro	Ser	Ser	Ser	Ser	Ser		
		420						425					430				
Ser	Ser	Val	Val	Asn	Asn	Gly	Ser	Ile	Ala	Leu	Thr	Ala	Thr	Ala	Thr		
		435				440						445					
Gly	Asn	Ser	Ile	Val	Leu	Ser	Trp	Ser	Pro	Asn	Asn	Leu	Thr	Leu	Gly		
	450					455				460							
Thr	Gln	Glu	Val	Tyr	Arg	Asp	Thr	Asp	Ser	Asp	Pro	Ser	Gly	Arg	Val		
465					470				475					480			
Arg	Ile	Ala	Ala	Leu	Ser	Ser	Ser	Thr	Arg	Met	Tyr	Thr	Asp	Ala	Thr		
			485					490					495				
Ala	Ser	Ala	Gly	Gln	Thr	Phe	Tyr	Tyr	Trp	Ile	Lys	Asn	Thr	Thr	Asn		
		500						505					510				
Gly	Val	Thr	Thr	Asn	Ser	Asn	Ala	Ala	Ser	Ala	Ala	Ile	Gly	Asp	Ala		
	515						520					525					
Ala	Arg	Ala	Ile	Arg	Ala	Cys	Ala	Gly	Asn	Arg	Gly	Ser	Gly	Ala	Arg		
	530					535					540						
Thr	Ser	Arg	Ala	Val	Ser	Thr	Gly	Ser	Asn	Pro	Arg	Gly	Pro	Ala	Gly		
545					550					555					560		
Ser	His	Pro	Arg	Ala													
				565													

<210> 89
 <211> 1377
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 89
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 60
 gcaccgcggt tcctggcggt ttcttcggtg gcgagtcctg gggaaacggt gatgccttcg
 120
 atcctcgaac gcatcaagcc accgcgtttt ccgaaacgca cgtgctatct caaccggttt
 180
 ggagcaaaaag gcgacgggca aactgattgc acttcagctt ttcgacgcgc aatcgatcag
 240
 tgttcgaaaag cgggcggtgg caaagtgatc gttccgcagg gaatgtatct caccggcgca
 300

attcacttga agagcaacgt caatctcgag atctccgaag gcgcgacgat caagttcagt
 360
 caaaacccga aagactatct cccggtggtt ttttcgcgtt gggaaggcgt cgaagtattc
 420
 aactactcac ctttcatcta cgcatttgaa cagcagaaca tcgcgatcac gggcaagggc
 480
 acgctcgatg ggcagagtga taacgaacac tgggtggccat ggaacggacg cgccagggtac
 540
 ggttggaag aaggggatgag ccaccagcgt ccggatcgaa acgcgctctt tgcgatggcg
 600
 gaaaaagggtg tttcggttcg cgaacgtggtt ttcggcgagg gtcattactt aaggccgcag
 660
 ttcattcagc cgtatcgctg ccagaacgta ttgatcgacg gagttacgat acgaaactcg
 720
 ccgatgtggg aaattcatcc ggtgctgtgc cggaatgtca tcgtgcaaaa cgtgcacatt
 780
 aacagtcatg gaccaaacia cgatggctgc aatcccagat cgtgcactga tgtgctgatt
 840
 aagaactgtt acttcgacac tggcgacgac tgtatcgcg tcaaatacagg acgcaacgcg
 900
 gacggccggc ggcttaaagc gccgacagag aacgtgatcg tgcaagactg tcaaataaaa
 960
 gatggacacg gcgggatcac tgtcggcagt gagatctcag gcggtgtgag aaatctgttt
 1020
 gcggagaact gccggcttga tagtccaaac ctggaccatg ctttgcgggt taagaacaac
 1080
 gcgatgcgtg gagggctgct cgagaatttg cacttccgaa acatcgaagt tggtcagggtg
 1140
 gcgcatgcag tgatcacgat cgattttaat tacgaggaag gcgcgaaagg atcgttcacg
 1200
 ccggtgggtc gtgactacac tgtcgatggt ttgcgcagca cgcaagcaa atacgcgctc
 1260
 gacgttcaag gtctgtcggg cgcgccgatc gtaaactctgc gtctgacgaa ttgcacgttc
 1320
 gacaatgttg ccgaagggaa cgtcgtgaag aatgttaagg acgcgacaat tcaaaaa
 1377

<210> 90
 <211> 459
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(31)

<221> DOMAIN
 <222> (32)...(459)
 <223> Catalytic domain

<400> 90
 Met Thr Thr Arg Arg Glu Phe Ile Arg Asp Leu Leu Val Gly Gly Val
 1 5 10 15
 Val Val Ala Val Ala Pro Arg Phe Leu Ala Phe Ser Ser Val Ala Ser
 20 25 30
 Pro Trp Glu Thr Val Met Pro Ser Ile Leu Glu Arg Ile Lys Pro Pro
 35 40 45
 Arg Phe Pro Lys Arg Thr Cys Tyr Leu Asn Arg Phe Gly Ala Lys Gly
 50 55 60

Asp	Gly	Gln	Thr	Asp	Cys	Thr	Ser	Ala	Phe	Arg	Arg	Ala	Ile	Asp	Gln
65					70					75				80	
Cys	Ser	Lys	Ala	Gly	Gly	Gly	Lys	Val	Ile	Val	Pro	Gln	Gly	Met	Tyr
				85					90					95	
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Ile	Ser
			100					105					110		
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asn	Pro	Lys	Asp	Tyr	Leu	Pro
		115					120					125			
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
	130					135					140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Gln	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
145					150					155					160
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Asn	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
			165						170					175	
Arg	Ala	Arg	Tyr	Gly	Trp	Lys	Glu	Gly	Met	Ser	His	Gln	Arg	Pro	Asp
			180					185					190		
Arg	Asn	Ala	Leu	Phe	Ala	Met	Ala	Glu	Lys	Gly	Val	Ser	Val	Arg	Glu
		195					200					205			
Arg	Val	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
	210					215					220				
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Asp	Gly	Val	Thr	Ile	Arg	Asn	Ser
225					230					235					240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Ile	Val	Gln
			245						250				255		
Asn	Val	His	Ile	Asn	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
			260					265					270		
Glu	Ser	Cys	Thr	Asp	Val	Leu	Ile	Lys	Asn	Cys	Tyr	Phe	Asp	Thr	Gly
		275					280					285			
Asp	Asp	Cys	Ile	Ala	Val	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
	290					295					300				
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Val	Ile	Val	Gln	Asp	Cys	Gln	Met	Lys
305					310					315					320
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
			325						330					335	
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
			340					345					350		
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
		355					360					365			
Asn	Leu	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala	Val
	370					375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385					390					395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Gly	Leu	Arg	Ser	Thr	Arg	Ser
			405						410					415	
Lys	Tyr	Ala	Leu	Asp	Val	Gln	Gly	Leu	Ser	Gly	Ala	Pro	Ile	Val	Asn
		420						425					430		
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asp	Asn	Val	Ala	Glu	Gly	Asn	Val
		435					440					445			
Val	Lys	Asn	Val	Lys	Asp	Ala	Thr	Ile	Gln	Lys					
	450					455									

<210> 91
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 91
 gtggtcctag gtaataacgg cggcagcttg agttgcgtcc aatatattgt gattgtgaaa

60
 ggacccggtg gacctcgacc gccggtgaaa ccggccgtcc aggcgcccgt taggggttacc
 120
 tggagcgcat ccctagtcca gcggcccga tggtagggga gtgacgaagc gatccgcatc
 180
 gcggacaacg tcctcctcta ccagcgcaac accggcgggt ggccgaagga catagatatg
 240
 gccgagccca tcccggaaca caggaagtcc tttttcctca ccgagaagga gcggaccgat
 300
 gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgc ccgctctac
 360
 aaggcgacca ggctggaacg gttcaaggag ggcttcctca aaggtctcga ctacctcttg
 420
 gccgcccagt acccgaacgg cggttgcccc cagtattatc ctaacttgag gggctactac
 480
 gccaacatca cttataacga caatgccatg gtgaacgtgc tcaccctcct ccagagcatc
 540
 gccaaaaagg ccccggaagta cgacttcgtc gaccggcgcc gccgggagaa ggccgcccgg
 600
 gccgtggcga aagggatcga ctgcatcctc aagaccaga tccgtgtcaa tggaaaactt
 660
 accgcctggt gcgcccagca tgacgccaag acgctggcgc ccgcgccggc ccgttcgtat
 720
 gagcttgagt ccatcagcgg tttcgagagc gtcgggatcg tccggttctt aatgagcctc
 780
 gagaatccga gcccggaaggt catcgaggcg gtagaggccg ccgtgaaatg gttcgaggag
 840
 gtcaagctta ccgggatcaa ggtggtcgag aaaccggacc cgtcccttcc gggcggttac
 900
 gaccgcgtgg tggtcgaaga cccaacgcg ccgcccattt gggcccgggt ctacgagatc
 960
 ggcaccaacc gtcccttctt ctgcggccgc gatggtatca aaaaatacag cctggcgagg
 1020
 atcgaacacg aacgccgggt cggttactcc tggtagacca atgccccggc ctacctcatc
 1080
 gagaaggagt atccgctctg gcgggcaaaa caccctacca agtaa
 1125

<210> 92
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(374)

<400> 92
 Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1 5 10 15
 Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
 20 25 30
 Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Ser Leu Val Gln Arg
 35 40 45
 Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
 50 55 60
 Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
 65 70 75 80
 Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys

				85					90					95					
Glu	Arg	Thr	Asp	Asp	Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Val	Thr	Gln				
			100					105					110						
Leu	Lys	Tyr	Leu	Ala	Arg	Val	Tyr	Lys	Ala	Thr	Arg	Leu	Glu	Arg	Phe				
		115					120					125							
Lys	Glu	Gly	Phe	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr				
		130				135					140								
Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Tyr	Pro	Asn	Leu	Arg	Gly	Tyr	Tyr				
145				150					155						160				
Ala	Asn	Ile	Thr	Tyr	Asn	Asp	Asn	Ala	Met	Val	Asn	Val	Leu	Thr	Leu				
			165					170						175					
Leu	Gln	Ser	Ile	Ala	Lys	Lys	Ala	Pro	Glu	Tyr	Asp	Phe	Val	Asp	Pro				
		180						185					190						
Ala	Arg	Arg	Glu	Lys	Ala	Ala	Arg	Ala	Val	Ala	Lys	Gly	Ile	Asp	Cys				
		195					200					205							
Ile	Leu	Lys	Thr	Gln	Ile	Arg	Val	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys				
	210					215					220								
Ala	Gln	His	Asp	Ala	Lys	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Ser	Tyr				
225				230				235						240					
Glu	Leu	Glu	Ser	Ile	Ser	Gly	Phe	Glu	Ser	Val	Gly	Ile	Val	Arg	Phe				
			245					250						255					
Leu	Met	Ser	Leu	Glu	Asn	Pro	Ser	Pro	Lys	Val	Ile	Glu	Ala	Val	Glu				
			260					265					270						
Ala	Ala	Val	Lys	Trp	Phe	Glu	Glu	Val	Lys	Leu	Thr	Gly	Ile	Lys	Val				
		275				280						285							
Val	Glu	Lys	Pro	Asp	Pro	Ser	Leu	Pro	Gly	Gly	Tyr	Asp	Arg	Val	Val				
	290					295					300								
Val	Glu	Asp	Pro	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile				
305				310				315						320					
Gly	Thr	Asn	Arg	Pro	Phe	Phe	Cys	Gly	Arg	Asp	Gly	Ile	Lys	Lys	Tyr				
			325					330					335						
Ser	Leu	Ala	Glu	Ile	Glu	His	Glu	Arg	Arg	Val	Gly	Tyr	Ser	Trp	Tyr				
			340					345					350						
Thr	Asn	Ala	Pro	Ala	Tyr	Leu	Ile	Glu	Lys	Glu	Tyr	Pro	Leu	Trp	Arg				
		355				360						365							
Ala	Lys	His	Pro	Thr	Lys														
	370																		

<210> 93
 <211> 1062
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 93
 gtggatccaa agaattggaa cccgaaaaaa gccgacgatt catggctcga aaagacgaaa
 60
 cccgattacc ggctgggtctc ctggcgcgac gttttagatc aaactcagct ctggtacgcg
 120
 gtcgacgaag cgacgcgcac cgccaaccag gttttgctct ttcagcgcgga taacggcggc
 180
 tgggaaaaaa acgtcgacat ggcgggcgatg ctcaactcaag ccgaacgaga aaaactcgtc
 240
 aaagaaaaat ctacaccgga tacgaccatc gacaacggcg cgacgaccac gcagctgcgt
 300
 tatctggcaa aagtcatcac ggcgaaaaac atcgaagctc ataaacagtc gtttctcaag
 360
 ggattggatt ttctgctcgc gatgcagtat gaaaacggag gatttccgca atattatcct
 420

ttgaaaaacg attattcgcg cgagattact ttcaacgacg acgcgatgat caatgttctt
 480
 aaattgctgc gcgacgtggc aaaaaagaag gaagattatt tattcgtcga cgaagaccgg
 540
 cgcgccagag cggaaggcgc ggtcgaaaaa ggcgtccgcc tgatcttgaa aacacaggtc
 600
 gccatcgacg gcaaaaaaac gatctgggcg gcgcagtacg acgaaaacac tttgaaaccg
 660
 gcaaattgcga gaaagtttga gcccgcctcg ctcgcttcgc gcgaatcggg cagcgtgggc
 720
 agatttttga tgctcgacgc caaaccgcgac gaggaaaaaa tcggagcgat cgaatcggcg
 780
 atcgaatggg ttcaaaaaaa caaactgagc ggcattcgct gggaatcgaa aagcggagaa
 840
 aacctggtcg tcaaagacaa agcggcgccg ccgatctggg gaaggtttta tcaattcgaa
 900
 accatgcgcc ccatttttat cgggcgcgac gcggtgattc gctacgatgt catgcaaadc
 960
 gaagccgaac gccgcaacgg ctacggctgg tacacgaacg agccgaacga gcttttggac
 1020
 aaagattatc cgaaatggaa agagaaaaatt aagaaaaatt ag
 1062

<210> 94
 <211> 353
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(353)

<400> 94
 Met Asp Pro Lys Asn Trp Asn Pro Lys Lys Ala Asp Asp Ser Trp Leu
 1 5 10 15
 Glu Lys Thr Lys Pro Asp Tyr Arg Leu Val Ser Trp Arg Asp Val Leu
 20 25 30
 Asp Gln Thr Gln Leu Trp Tyr Ala Val Asp Glu Ala Thr Arg Ile Ala
 35 40 45
 Asn Gln Val Leu Leu Phe Gln Arg Asp Asn Gly Gly Trp Glu Lys Asn
 50 55 60
 Val Asp Met Ala Ala Met Leu Thr Gln Ala Glu Arg Glu Lys Leu Val
 65 70 75 80
 Lys Glu Lys Ser His Thr Asp Thr Thr Ile Asp Asn Gly Ala Thr Thr
 85 90 95
 Thr Gln Leu Arg Tyr Leu Ala Lys Val Ile Thr Ala Lys Asn Ile Glu
 100 105 110
 Ala His Lys Gln Ser Phe Leu Lys Gly Leu Asp Phe Leu Leu Ala Met
 115 120 125
 Gln Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Leu Lys Asn Asp
 130 135 140
 Tyr Ser Arg Glu Ile Thr Phe Asn Asp Asp Ala Met Ile Asn Val Leu
 145 150 155 160
 Lys Leu Leu Arg Asp Val Ala Lys Lys Lys Glu Asp Tyr Leu Phe Val
 165 170 175
 Asp Glu Asp Arg Arg Ala Arg Ala Glu Gly Ala Val Glu Lys Gly Val
 180 185 190
 Arg Leu Ile Leu Lys Thr Gln Val Ala Ile Asp Gly Lys Lys Thr Ile
 195 200 205

Trp Ala Ala Gln Tyr Asp Glu Asn Thr Leu Lys Pro Ala Asn Ala Arg
 210 215 220
 Lys Phe Glu Pro Ala Ser Leu Ala Ser Arg Glu Ser Val Ser Val Val
 225 230 235 240
 Arg Phe Leu Met Leu Asp Ala Lys Pro Asp Glu Glu Lys Ile Gly Ala
 245 250 255
 Ile Glu Ser Ala Ile Glu Trp Phe Gln Lys Asn Lys Leu Ser Gly Ile
 260 265 270
 Arg Trp Glu Ser Lys Ser Gly Glu Asn Leu Val Val Lys Asp Lys Ala
 275 280 285
 Ala Pro Pro Ile Trp Gly Arg Phe Tyr Gln Phe Glu Thr Met Arg Pro
 290 295 300
 Ile Phe Ile Gly Arg Asp Ala Val Ile Arg Tyr Asp Val Met Gln Ile
 305 310 315 320
 Glu Ala Glu Arg Arg Asn Gly Tyr Gly Trp Tyr Thr Asn Glu Pro Asn
 325 330 335
 Glu Leu Leu Asp Lys Asp Tyr Pro Lys Trp Lys Glu Lys Ile Lys Lys
 340 345 350
 Asn

<210> 95
 <211> 1074
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 95
 atgacgctac ccgttggttc cctgcgcgta ctgctggcgc tgctggccac gtcgccggtc
 60
 gcctgcgcgg gcgccgcggc acccgcgact gcgaccgatc cggtcgccga gaacatgctg
 120
 cttctgcaga ccgcctccgg cggctggtcc aagcactacc gcgagaagaa ggtcgactac
 180
 gcgcgcgact acgacgccgc cgagcgcgcc gcgctgcgcg cgcccgaccg gcatgacgat
 240
 gcgacgatcg acaacaaggc cacgaccacc gagatcgctt acctggtgca ggcacatgcc
 300
 aggacgggca atccggccta cctcgacggc gcgcgccgcg gcgtcgagta cctgctgcgc
 360
 gcccagtacc cgaacggcgg ctggccgcag ttctaccccg accattcgct ctaccggcac
 420
 cagatcacgc tcaacgacga tgcgatggtg cacgccatca ccgtgctgca ggacatcgcc
 480
 gcggggccgca acggcatgca ggtgctggcg ccggagttcg gcgtccgcgc cgccgcggcc
 540
 gcgcagcgcg gcatcgaaa cctgctcgag ttgcaggtgc ggatcgccgg ggtgccgacg
 600
 atatgggccg cgcagtacga cgagaccagc ctgcaaccgg ccaaggcccc cgcgtagcaa
 660
 ctgccttcgc tggccgtggc cgaatcggtc ggcgtggtgc gcctgctgat gcgccagccg
 720
 gcgcctgatg cgcgcacggt cgccgcgacg gaggcggcgg ccgactggct ggaggcgcac
 780
 cgccctgccg acctcgccct ggaacgcacg gaagcccccg ccgaggaaac cggcaaggac
 840
 gtccgcgtcg tggccagacc gggcgcgtcg ttgtgggcgc gcttctacga cctcgagcgg
 900
 caggtgccgc tggtcgtcga tcgcaacagc cgctccgtgc ccttcgccga gcttcccaac

960
gagcgtcgta cccgctatgg ctggtatggc acctggccgg aaaagctgct ggcacaggaa
1020
ctccccgcgt ggcgcaaggt ccatgcggcc agcgcgggcg ctccggcccg ttga
1074

<210> 96
<211> 357
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(357)
<223> Catalytic domain

<400> 96
Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
1 5 10 15
Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
20 25 30
Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
35 40 45
Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
50 55 60
Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp
65 70 75 80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Thr Glu Ile Ala Tyr Leu Val
85 90 95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
100 105 110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
115 120 125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
130 135 140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145 150 155 160
Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
165 170 175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
180 185 190
Val Arg Ile Ala Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
195 200 205
Thr Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
210 215 220
Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
225 230 235 240
Ala Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ala Ala Ala Asp Trp
245 250 255
Leu Glu Ala His Arg Leu Pro Asp Leu Ala Leu Glu Arg Ile Glu Ala
260 265 270
Pro Ala Glu Thr Gly Lys Asp Val Arg Val Val Ala Arg Pro Gly
275 280 285
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Glu Arg Gln Val Pro Leu
290 295 300
Phe Val Asp Arg Asn Ser Arg Pro Val Pro Phe Ala Glu Leu Pro Asn

305					310					315				320
Glu	Arg	Arg	Thr	Gly	Tyr	Gly	Trp	Tyr	Gly	Thr	Trp	Pro	Glu	Lys
				325					330					335
Leu	Ala	Gln	Glu	Leu	Pro	Arg	Trp	Arg	Lys	Val	His	Ala	Ala	Ser
			340					345					350	
Gly	Ala	Pro	Ala	Arg										
			355											

<210> 97
 <211> 2097
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 97
 ttgaacgccg ccggcagccg gcggttcgcg caactcgtcg tcgcggatct gcggcggctg
 60
 gtgcccgcgc tggcgccctt ctttcgcgac gagccgctgg cgggaggagt cgccgcgctc
 120
 cagcgcagcg tcgatgcgat cgtcgccgcg gacggcaccg gacagtttgc gacggtgcag
 180
 gaggcgatca acgccgcgcc gcagaacacc agcacgacca gccgctggat catcctcgtc
 240
 aaaccaggca cgtatcgcgga ggtcgtctac gtgcagcgtg agaagcgctt cgtcacgctg
 300
 atcggcgaag acccggcacg gacgacgac acgtaccacc tcaaagcgtc tgacgtgggg
 360
 ctcgacggca agcccatcgg cacgtttcgc acgccgacga tgggtggtgga tgccgacgat
 420
 ttcacgatcg agaacctcac catcgagaac ggggcagggc cggtcggtca agcgtgggc
 480
 ttgcgagtgg acggcgatcg cgtgacgggtg aggaacagcc gcctgctggg ctggcaggac
 540
 acgatctttc tcaaccgtgg gcgccactac ttcgaggact cgttcacgcg cgggcacgtg
 600
 gatttcatth tcggcgggcg gacggcggtg ttcgagcgat gccatcttcg cgctggcg
 660
 gacggctacc tcacggccgc gtccacgccc gcggagcaac gattcggctt cgtgttcctg
 720
 aacagcatcg tcagtggaga agctggcgcc cgcacgtacc tcggtcgacc gtggcgggcg
 780
 ttcgcgcacg tggccttcat caagacgacg atgggcgagg tgggtgcgcc ggtgggctgg
 840
 aacaactggg accggccgga gcgtgagaag accgtgcgtt ttctcgaagc aggcaccagc
 900
 ggcgcggggc gcagcgtcgc tgcgcgcgtc gcctgggcgc gcgtcgccac gccagccgag
 960
 ctcgctgacg tgacgaccga ggtggtgctt ggcggcaccg acggtgga cccgcgtcgc
 1020
 gtcgccccgt acccgtcggc cgttcgcgcc aacgcggcg cgctgccgc gccgcccggg
 1080
 cccgacgtcg ctggcccga gagcccgccc gccttgacgt gggaccaggt cgcgcgccag
 1140
 ccagcgtcgt ggctggccac acccgaagcg ctgcggattg ccgagaacgt gcgcctctat
 1200
 caacggcaca ctggcggtg gcccaaaaac ctcgacatgg cgcagccgtt gacggacgcc
 1260
 gatcgcgcgc gtctcacggc cgatcgcgcg ctcgacgact cgaccatcga caatggcgcc
 1320

acgacgcggc agatcgagtt tctcgcccgg atcgccgccc ccaaccgcga cgagcgcgcg
 1380
 caggcgtcga tgctggctgg gatcgactac ctgctcgcgg cccagtatcc aaacggcggc
 1440
 tggccgcagt atttcccgt cgcgaacgac tactcgcgcc acatcacgtt caacgacgac
 1500
 gcgatgatcg cggccgcgac gatcctgcag tcggtcgcg c tggcccgtcc gccgttcgcc
 1560
 ggcgtcgacg cgactcgccc cggcgggcg gcggaggccg tcgcgcgcg ccacgcgctg
 1620
 attctggcct cgcagattcg cgtcaacggc cagctcactg gctggtgcc a gcagcacgat
 1680
 gcacgcacgc tggagccagc gcgcggggcg acctacgagc atccatcgat cagtggccgc
 1740
 gaaaccgtga cgatcgtcaa tttcctgcgg tcgatcgaac cgcgcgaccg ccagacccaa
 1800
 gccgccatcg atgccgcgat ggagtggctc aaggccgtgc agatccgcgg ctggcgacg
 1860
 gagcggcggc ccgatccctc aggaccgggc ggttacgacg tggatgatgt ggaggacccc
 1920
 aacgcggcgc cgctctgggc ccgcttctac gagattggca ccaatcgtcc gatctactcg
 1980
 ggccgggacg gcgtcatcaa gtaccggctc gccgagatcg aaattgaacg gcggaccggc
 2040
 tacagctggg tcggaccgta cgcgcaggcg ctgctcgatg aagagcgcag gaagtaa
 2097

<210> 98
 <211> 698
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (45)...(333)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (336)...(698)
 <223> Catalytic domain

<400> 98
 Met Asn Ala Ala Gly Ser Arg Arg Phe Ala Gln Leu Val Val Ala Asp
 1 5 10 15
 Leu Arg Arg Leu Val Pro Ala Leu Ala Pro Phe Phe Arg Asp Glu Pro
 20 25 30
 Leu Ala Gly Gly Val Ala Ala Leu Gln Arg Ser Val Asp Ala Ile Val
 35 40 45
 Ala Ala Asp Gly Thr Gly Gln Phe Ala Thr Val Gln Glu Ala Ile Asn
 50 55 60
 Ala Ala Pro Gln Asn Thr Ser Thr Thr Ser Arg Trp Ile Ile Leu Val
 65 70 75 80
 Lys Pro Gly Thr Tyr Arg Glu Val Val Tyr Val Gln Arg Glu Lys Arg
 85 90 95
 Phe Val Thr Leu Ile Gly Glu Asp Pro Ala Arg Thr Thr Ile Thr Tyr
 100 105 110
 His Leu Lys Ala Ser Asp Val Gly Leu Asp Gly Lys Pro Ile Gly Thr
 115 120 125
 Phe Arg Thr Pro Thr Met Val Val Asp Ala Asp Asp Phe Thr Ile Glu

	130					135					140					
Asn 145	Leu	Thr	Ile	Glu	Asn 150	Gly	Ala	Gly	Pro	Val 155	Gly	Gln	Ala	Leu	Ala 160	
Leu	Arg	Val	Asp	Gly 165	Asp	Arg	Val	Thr	Val 170	Arg	Asn	Ser	Arg	Leu 175	Leu	
Gly	Trp	Gln	Asp 180	Thr	Ile	Phe	Leu	Asn 185	Arg	Gly	Arg	His	Tyr 190	Phe	Glu	
Asp	Ser	Phe 195	Ile	Gly	Gly	His	Val 200	Asp	Phe	Ile	Phe	Gly 205	Gly	Ala	Thr	
Ala	Val 210	Phe	Glu	Arg	Cys	His 215	Leu	Arg	Ala	Trp	Arg 220	Asp	Gly	Tyr	Leu	
Thr 225	Ala	Ala	Ser	Thr	Pro 230	Ala	Glu	Gln	Arg	Phe 235	Gly	Phe	Val	Phe	Leu 240	
Asn	Ser	Ile	Val	Ser 245	Gly	Glu	Ala	Gly	Ala 250	Arg	Thr	Tyr	Leu	Gly 255	Arg	
Pro	Trp	Arg	Ala 260	Phe	Ala	His	Val	Ala 265	Phe	Ile	Lys	Thr	Thr 270	Met	Gly	
Glu	Val	Val	Arg 275	Pro	Val	Gly	Trp 280	Asn	Asn	Trp	Asp	Arg 285	Pro	Glu	Arg	
Glu	Lys 290	Thr	Val	Arg	Phe	Leu 295	Glu	Ala	Gly	Thr	Ser 300	Gly	Ala	Gly	Gly	
Ser 305	Val	Ala	Ala	Arg	Val 310	Ala	Trp	Ala	Arg	Val 315	Ala	Thr	Pro	Ala	Glu 320	
Leu	Ala	Asp	Leu	Thr 325	Thr	Glu	Val	Val	Leu 330	Gly	Gly	Thr	Asp	Gly 335	Trp	
Asp	Pro	Arg	Arg 340	Val	Ala	Pro	Tyr	Pro 345	Ser	Ala	Val	Arg	Ala 350	Asn	Ala	
Ala	Pro	Leu 355	Pro	Arg	Pro	Pro	Gly 360	Pro	Asp	Val	Ala	Gly 365	Pro	Gln	Ser	
Pro	Pro 370	Ala	Leu	Thr	Trp	Asp 375	Gln	Val	Ala	Arg	Gln 380	Pro	Ala	Ser	Trp	
Leu 385	Ala	Thr	Pro	Glu	Ala 390	Leu	Arg	Ile	Ala	Glu 395	Asn	Val	Arg	Leu	Tyr 400	
Gln	Arg	His	Thr	Gly 405	Gly	Trp	Pro	Lys	Asn 410	Leu	Asp	Met	Ala	Gln 415	Pro	
Leu	Thr	Asp	Ala 420	Asp	Arg	Ala	Arg	Leu 425	Thr	Ala	Asp	Arg	Ala 430	Leu	Asp	
Asp	Ser	Thr 435	Ile	Asp	Asn	Gly	Ala 440	Thr	Thr	Arg	Gln	Ile 445	Glu	Phe	Leu	
Ala	Arg	Ile	Ala	Ala	Ala	Asn 455	Arg	Asp	Glu	Arg	Ala	Gln	Ala	Ser	Met	
Leu 465	Ala	Gly	Ile	Asp	Tyr 470	Leu	Leu	Ala	Ala	Gln 475	Tyr	Pro	Asn	Gly	Gly 480	
Trp	Pro	Gln	Tyr	Phe 485	Pro	Leu	Arg	Asn	Asp 490	Tyr	Ser	Arg	His	Ile 495	Thr	
Phe	Asn	Asp	Asp 500	Ala	Met	Ile	Ala	Ala 505	Ala	Thr	Ile	Leu	Gln 510	Ser	Val	
Ala	Leu	Ala	Arg 515	Pro	Pro	Phe	Ala 520	Gly	Val	Asp	Ala	Thr 525	Arg	Arg	Arg	
Arg	Ala 530	Ala	Glu	Ala	Val	Ala 535	Arg	Ala	His	Arg	Val 540	Ile	Leu	Ala	Ser	
Gln 545	Ile	Arg	Val	Asn	Gly 550	Gln	Leu	Thr	Gly	Trp 555	Cys	Gln	Gln	His	Asp 560	
Ala	Arg	Thr	Leu	Glu 565	Pro	Ala	Arg	Gly	Arg 570	Thr	Tyr	Glu	His	Pro 575	Ser	
Ile	Ser	Gly	Arg 580	Glu	Thr	Val	Thr	Ile	Val 585	Asn	Phe	Leu	Arg	Ser	Ile	
Glu	Pro	Arg 595	Asp	Arg	Gln	Thr	Gln	Ala	Ala	Ile	Asp	Ala 605	Ala	Met	Glu	
Trp	Leu	Lys	Ala	Val	Gln	Ile 615	Arg	Gly	Trp	Arg	Thr 620	Glu	Arg	Arg	Pro	

Asp	Pro	Ser	Gly	Pro	Gly	Gly	Tyr	Asp	Val	Val	Met	Val	Glu	Asp	Pro
625					630					635					640
Asn	Ala	Ala	Pro	Leu	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg
				645					650					655	
Pro	Ile	Tyr	Ser	Gly	Arg	Asp	Gly	Val	Ile	Lys	Tyr	Arg	Leu	Ala	Glu
			660					665					670		
Ile	Glu	Ile	Glu	Arg	Arg	Thr	Gly	Tyr	Ser	Trp	Val	Gly	Pro	Tyr	Ala
		675					680					685			
Gln	Ala	Leu	Leu	Asp	Glu	Glu	Arg	Arg	Lys						
	690					695									

<210> 99
 <211> 1782
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 99
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 120
 ttttcgacca cggatggcgg caatgtgtca gggcaaaaat cctttaccgc ctcaagccac
 180
 acccaaatcc agcaaatcct tgaggatgcc aaagatggca attatccggt ggtgatcacc
 240
 tacaccggca atgaggattc actgattaac caagtcgtcc gggatcacac cgtcgattct
 300
 tcaggcaact gccctaaagc gcgttggaaat gatgcctacc gcaaagtcga aatcaaagaa
 360
 atgaccaagg gtgtcaccat tcagggtgcc aatggttcgt cggcgaattt cggaatcgtg
 420
 gtgaataaat ccagcaacgt gattattcgc aacatgaaga ttggtgcact gggcggcgct
 480
 aataacgatg cggatatgat ccgtgtggac agcgggtgtga acgtctggat cgatcacaac
 540
 gaattattcg ccgtgaacaa cgagtgtgaag gggtcaccgc atggcgatct gacctttgaa
 600
 agcgcgattg atatcaaaaa agcctcgcaa gatatcaccg tgcctacaa cgtgattcgc
 660
 gacagtaaaa aagtcggttt ggatggctcc agcagcagcg atatcgccgg cggccgcaaa
 720
 attactttcc accacaatat ctaccgcaac gtaggtgcgc gcttaccttt gcagcgcggc
 780
 ggttggacgc acatgtacaa caacctgtac gacggcatta ccagctcggg catcaacgtg
 840
 cgccaaaacg gttatgcgtt aattgaaagc aactgggttc aaaacgcggt taaccgcggtc
 900
 acctgccgtt ttgacagcag caactgcggc aagtgggatc tgcgcaacaa taacatccgc
 960
 aaccgggtg attttgcgac ttacaacatc acctggacca gtggcggcac catcgacgcc
 1020
 accaactgga ccaccactgc gcccttccct atcagcattc cctacagcta ttcaccggtt
 1080
 actccgcaat gtgtgaaaga tcgtctggcg agttacgcgg gtgtgggtaa aaacggcgcg
 1140
 cagctgactg cctcggcctg cgggtggtcg gcacgttcca cacctgcac gtccacaccc
 1200
 gcaagttcca gctctgcggc aaacagttcc gctgcatcag gcagtgtgag tttgggtggc

1260
 agtgccggtg atgcatcggt tgcacttaac tggaccgtga atgccaacat taatgcgctg
 1320
 gaaatttatc aggatacggg ttctgatccc gccggacgtg tgcgcattgc gtcgctgcca
 1380
 accagcgga ccaactacac cgcaacaggt ctgagcaacg gcactaccta ttacttctgg
 1440
 gtgaaatata gcaccaccaa taatgtgtgg agcaactcca atgtgttcag cgccaagcca
 1500
 agttcaggta caaccccgct atcatccagc agcgcggctt catcaacgcc aagtgggtga
 1560
 ccggtgttaa gtggtacagg tgattaccca agcggcttct ccaagtgtgc tgatctgggt
 1620
 ggacactgct cagtcgcctc gggcgatggt tgggtgcct ttggtcgcaa aggcaagtgg
 1680
 gtcacaaaaa aagtgtcagt cggtagctct attgcctgta ccgttgccgc gtttgatct
 1740
 gatccacaag gcaatcccaa taagtgttct tataaaaaagt aa
 1782

<210> 100
 <211> 593
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(35)

<221> DOMAIN
 <222> (36)...(593)
 <223> Catalytic domain

<400> 100
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 1 5 10 15
 Ser Leu Thr Ala Met Ala Ala Ala Val Ala Met Ile Ala Gly Thr Ser
 20 25 30
 Ala Phe Ala Ala Ser Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
 35 40 45
 Val Ser Gly Ser Lys Ser Phe Thr Ala Ser Ser His Thr Gln Ile Gln
 50 55 60
 Gln Ile Leu Glu Asp Ala Lys Asp Gly Asn Tyr Pro Val Val Ile Thr
 65 70 75 80
 Tyr Thr Gly Asn Glu Asp Ser Leu Ile Asn Gln Val Val Arg Asp His
 85 90 95
 Thr Val Asp Ser Ser Gly Asn Cys Pro Lys Ala Arg Trp Asn Asp Ala
 100 105 110
 Tyr Arg Lys Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Gln
 115 120 125
 Gly Ala Asn Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser
 130 135 140
 Ser Asn Val Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Gly Gly Ala
 145 150 155 160
 Asn Asn Asp Ala Asp Met Ile Arg Val Asp Ser Gly Val Asn Val Trp
 165 170 175
 Ile Asp His Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser
 180 185 190
 Pro Asp Gly Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Ala

atgactatag accgtcgaga attccttata gacctcatta tcggcaccgc cggcttcgca
 60
 atcgcaccga gtgatgcgtt cggccaagct gatccatgga aaaccgtcta tccgcaaadc
 120
 ctgcgtcgca tacggccacc gaaatttccg aagcgagatt tcatcatcac tagattcggc
 180
 gcaaagccgg gaaccgacag cgccgctgcy atcgcaaaaag ctatcaccgc gtgcagcaag
 240
 gcaggcggag gacgtgttct cgttcccgcga ggagagtctc tcaccggagc gatccatctg
 300
 aaatcgaacg taaactttca cgtgtcaaaa ggcgcgacgc tgaaattctc gaccgacccg
 360
 aaggcatatc tcccgattgt acatacgcga tgggaaggaa tggagctgat gcattctgtca
 420
 ccgttcattc acgcttatga gcagacgaac atcgctatca cgggtcaggg aacgctcgac
 480
 ggccaggga aatcattctt ctggaaatgg catggcaatc cggcttatgg cggcgatccg
 540
 aacacgctca gccaacggcc cgctcgtgcy cggctttacg agatgatgga taagaatgtg
 600
 ccggtcgcgc aacgtgtctt cggctcgcga cattatctgc ggccgcagtt tattcagccg
 660
 tacaaatgca ggaacgtttt gatcgaagat gtgacgatcy tcgattcgcg gatgtgggaa
 720
 gttcatccgg tgctttgcga gaacgtcacg gtccgaaatg ttcacatttc atcgcatggt
 780
 ccgaacaatg acggatgcga tccggagtcg tgcaaggacg tactgatcga caactgtttt
 840
 ttcgacaccg gcgacgattg catcgcgacg aagtcgggcc gcaacaatga cggctcgcgc
 900
 atcaatgtcc cgaccgagaa catcatcgtc cgcaactgca caatgaaaga cggctcatggc
 960
 ggcatcacgg tcggcagtgat gatttcggga ggctgcgaa atctttttgc gcacgattgt
 1020
 cgactcgaca gtgcggatct ctggaccgcg ctctcgcgtc agaacaatgc gtcgcgaggc
 1080
 ggcaagctcg agaattttta ttttcggaat ataacggtcg gccaggtcgc acgcgctgtg
 1140
 gtcgagatcg attttaatta cgaggaaggc gcgaaaggct cgtatatccg tctcgttcga
 1200
 aattatgttg ttgaaggact gacatgcgcc acaggcaatc gcgccgtcga tctgcaagga
 1260
 ttggacaacg cgccgatcta caatgtaacg ctgcgaaact gtacgtttgg ttctgtccga
 1320
 aatcgtagtg ttgtgaaaaa cgttcgtgga ctccggctcg agaatgtgaa gatcggcggc
 1380
 aggatcgtaa acgaactggc atga
 1404

<210> 102

<211> 467

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (78)...(459)
<223> Catalytic domain

<400> 102

Met	Thr	Ile	Asp	Arg	Arg	Glu	Phe	Leu	Ile	Asp	Leu	Ile	Ile	Gly	Thr
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Ala	Gly	Phe	Ala	Ile	Ala	Pro	Ser	Asp	Ala	Phe	Gly	Gln	Ala	Asp	Pro
			20					25					30		
Trp	Lys	Thr	Val	Tyr	Pro	Gln	Ile	Leu	Ala	Arg	Ile	Arg	Pro	Pro	Lys
		35				40						45			
Phe	Pro	Lys	Arg	Asp	Phe	Ile	Ile	Thr	Arg	Phe	Gly	Ala	Lys	Pro	Gly
	50					55					60				
Thr	Asp	Ser	Ala	Ala	Ala	Ile	Ala	Lys	Ala	Ile	Thr	Ala	Cys	Ser	Lys
65					70					75				80	
Ala	Gly	Gly	Gly	Arg	Val	Leu	Val	Pro	Ala	Gly	Glu	Phe	Leu	Thr	Gly
				85					90					95	
Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Phe	His	Val	Ser	Lys	Gly	Ala
			100					105					110		
Thr	Leu	Lys	Phe	Ser	Thr	Asp	Pro	Lys	Ala	Tyr	Leu	Pro	Ile	Val	His
		115				120						125			
Thr	Arg	Trp	Glu	Gly	Met	Glu	Leu	Met	His	Leu	Ser	Pro	Phe	Ile	Tyr
	130					135						140			
Ala	Tyr	Glu	Gln	Thr	Asn	Ile	Ala	Ile	Thr	Gly	Gln	Gly	Thr	Leu	Asp
145					150					155					160
Gly	Gln	Gly	Lys	Ser	Phe	Phe	Trp	Lys	Trp	His	Gly	Asn	Pro	Ala	Tyr
				165					170					175	
Gly	Gly	Asp	Pro	Asn	Thr	Leu	Ser	Gln	Arg	Pro	Ala	Arg	Ala	Arg	Leu
			180					185					190		
Tyr	Glu	Met	Met	Asp	Lys	Asn	Val	Pro	Val	Ala	Glu	Arg	Val	Phe	Gly
		195					200					205			
Leu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro	Tyr	Lys	Cys	Arg
	210					215					220				
Asn	Val	Leu	Ile	Glu	Asp	Val	Thr	Ile	Val	Asp	Ser	Pro	Met	Trp	Glu
225					230					235					240
Val	His	Pro	Val	Leu	Cys	Glu	Asn	Val	Thr	Val	Arg	Asn	Val	His	Ile
				245						250				255	
Ser	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asp	Pro	Glu	Ser	Cys	Lys
			260					265					270		
Asp	Val	Leu	Ile	Asp	Asn	Cys	Phe	Asp	Thr	Gly	Asp	Asp	Cys	Ile	
		275					280					285			
Ala	Ile	Lys	Ser	Gly	Arg	Asn	Asp	Gly	Arg	Arg	Ile	Asn	Val	Pro	
	290					295					300				
Thr	Glu	Asn	Ile	Ile	Val	Arg	Asn	Cys	Thr	Met	Lys	Asp	Gly	His	Gly
305					310					315					320
Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val	Arg	Asn	Leu	Phe
				325					330					335	
Ala	His	Asp	Cys	Arg	Leu	Asp	Ser	Ala	Asp	Leu	Trp	Thr	Ala	Leu	Arg
			340					345					350		
Val	Lys	Asn	Asn	Ala	Ser	Arg	Gly	Lys	Leu	Glu	Asn	Phe	Tyr	Phe	
		355					360					365			
Arg	Asn	Ile	Thr	Val	Gly	Gln	Val	Ala	Arg	Ala	Val	Val	Glu	Ile	Asp
	370					375					380				
Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Tyr	Ile	Pro	Val	Val	Arg
385					390					395					400
Asn	Tyr	Val	Val	Glu	Gly	Leu	Thr	Cys	Ala	Thr	Gly	Asn	Arg	Ala	Val
				405					410					415	
Asp	Leu	Gln	Gly	Leu	Asp	Asn	Ala	Pro	Ile	Tyr	Asn	Val	Thr	Leu	Arg
		420						425					430		
Asn	Cys	Thr	Phe	Gly	Ser	Val	Arg	Asn	Arg	Ser	Val	Val	Lys	Asn	Val
		435					440					445			
Arg	Gly	Leu	Arg	Leu	Glu	Asn	Val	Lys	Ile	Gly	Gly	Arg	Ile	Val	Asn

450
Glu Leu Val
465

455

460

<210> 103
<211> 1101
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 103
atgaacaccg cactgcaccg cgtcatccgc ctgccgctgc tgctggcgct gtgctgccc
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gcgctgcagg cacaggccac gcagaccgag cccgtcgccg agaacatgct gctgctgcag
120
accgctccg gcggctggc caagcaccac cagggaagg cggtcgacta cgccacacg
180
ttcaccgatg ccgaacgtgc ggcgctgcgc gcgcccgacc gcagggacga tgcgacgatc
240
gacaacaagg cgaccacgct tgagatcgtc gcgctgctgg aagcccacca gcgcaccggc
300
aatgccgcct atctggcggc tgcgcagcgc ggcgctggact acctgctggc cgcgcagtac
360
ccgaacggcg gctggccgca gtactaccgc gaccgttcgc tgtaccggca ccaggtcacc
420
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480
ggcgcgctgg cgcagctgac acccacgcat ggcgaaacgc ccagggccgc gctcgacagg
540
ggcatcgcct gcgtgctcgc caccaggtta cggatcgatg gcgagctcac gctctgggccc
600
gcgcagtagc acgaagccac gctgcagccg gcgaaggcgc gtccttacga gctgccatcg
660
ctggcggtcg ccgaatcggc cggggtgatg cggctgctga tgcgccagcc acagccgtcg
720
ccgcaggtgc tgacggcggc cgaggccggc gcacgctggc tggaggcgca ccgatgcgc
780
gacctggccc ggcgaaagat cgacgcgccc ggcgaaagaa ccggccagga cgtggtgatc
840
gtcgccgagc ccggcgcgtc gctgtgggca cgcttctacg acctgcagca ccagcagccg
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960
cggtcggct acgcctggta tggcgtgtgg ccggagaagc tgctgcagca ggagctgcca
1020
cgctggtaca acacccatgc cgaggcattg cgcgcgatta cgctgcgca tgccgagcca
1080
aggccgccga agcggccctg a
1101

<210> 104
<211> 366
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(26)

<221> DOMAIN

<222> (27)...(366)

<223> Catalytic domain

<400> 104

Met	Asn	Thr	Ala	Leu	His	Arg	Val	Ile	Arg	Leu	Pro	Leu	Leu	Leu	Ala
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Leu	Cys	Leu	Pro	Ala	Leu	Gln	Ala	Gln	Ala	Thr	Gln	Thr	Glu	Pro	Val
			20					25					30		
Ala	Glu	Asn	Met	Leu	Leu	Leu	Gln	Thr	Ala	Ser	Gly	Gly	Trp	Ser	Lys
		35					40					45			
His	His	Gln	Gly	Lys	Ala	Val	Asp	Tyr	Gly	His	Thr	Phe	Thr	Asp	Ala
	50					55					60				
Glu	Arg	Ala	Ala	Leu	Arg	Ala	Pro	Asp	Arg	Arg	Asp	Asp	Ala	Thr	Ile
65					70				75						80
Asp	Asn	Lys	Ala	Thr	Thr	Leu	Glu	Ile	Val	Ala	Leu	Leu	Glu	Ala	His
				85					90					95	
Gln	Arg	Thr	Gly	Asn	Ala	Ala	Tyr	Leu	Ala	Ala	Ala	Gln	Arg	Gly	Val
		100						105					110		
Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr
	115						120					125			
Tyr	Pro	Asp	Arg	Ser	Leu	Tyr	Arg	His	Gln	Val	Thr	Phe	Asn	Asp	Asp
	130					135					140				
Ala	Met	Thr	Arg	Val	Leu	Glu	Leu	Leu	Gln	Asp	Ile	Val	Glu	Gly	Lys
145					150				155						160
Gly	Ala	Leu	Ala	Gln	Leu	Thr	Pro	Thr	His	Gly	Glu	Arg	Ala	Arg	Ala
				165					170					175	
Ala	Leu	Asp	Arg	Gly	Ile	Ala	Cys	Val	Leu	Ala	Thr	Gln	Val	Arg	Ile
		180						185					190		
Asp	Gly	Glu	Leu	Thr	Leu	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Ala	Thr	Leu
	195						200					205			
Gln	Pro	Ala	Lys	Ala	Arg	Ser	Tyr	Glu	Leu	Pro	Ser	Leu	Ala	Val	Ala
	210					215					220				
Glu	Ser	Val	Gly	Val	Met	Arg	Leu	Leu	Met	Arg	Gln	Pro	Gln	Pro	Ser
225					230				235						240
Pro	Gln	Val	Leu	Thr	Ala	Val	Glu	Ala	Gly	Ala	Arg	Trp	Leu	Glu	Ala
				245					250					255	
His	Arg	Met	Arg	Asp	Leu	Ala	Arg	Arg	Lys	Ile	Asp	Ala	Pro	Gly	Glu
		260						265					270		
Glu	Thr	Gly	Gln	Asp	Val	Val	Ile	Val	Ala	Glu	Pro	Gly	Ala	Ser	Leu
	275						280					285			
Trp	Ala	Arg	Phe	Tyr	Asp	Leu	Gln	His	Gln	Gln	Pro	Met	Phe	Val	Asn
	290					295					300				
Arg	Glu	Gly	Glu	Gln	Val	Ala	Arg	Phe	Ala	Asp	Met	Pro	Asn	Glu	Arg
305					310					315					320
Arg	Val	Gly	Tyr	Ala	Trp	Tyr	Gly	Val	Trp	Pro	Glu	Lys	Leu	Leu	Gln
			325						330					335	
Gln	Glu	Leu	Pro	Arg	Trp	Tyr	Asn	Thr	His	Ala	Glu	Ala	Leu	Arg	Ala
		340						345					350		
Ile	Thr	Pro	Ala	His	Ala	Glu	Pro	Arg	Pro	Pro	Lys	Arg	Pro		
		355					360					365			

<210> 105

<211> 1203

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 105
 atgcaattca tcgaaacaca gcaattgggg accgccgcga aaccctgtggc gggacgagga
 60
 ggcgacaggc gctttccgcg ggtcatgccc gccgtttgcg cgggccttgc cctcgccgtg
 120
 tcgtcggccg agccggtccg ggcgagggc gcggatgcgg atgcggatgg cccactgccc
 180
 aggtggaaca ggaggctggg ggatcgcccc gaggactggg tcgcctccga cgagggacag
 240
 cgcgttgccg ccaacgtcct ccgctaccaa tcggcggaag gagcctggcc caaaaacacc
 300
 aatctggccg ccactcccc tgcctccgag gacattccct cctcgacctc cggggtggcc
 360
 aacacgatcg acaatgaagc caccaccgtg cccattcggg ttttgccccg tttcgcgcaa
 420
 atcaacgagg acacggccag ccgcgaggcg gtcgagcgcg gattggacta tctcctcaag
 480
 gcgcaatatt cgaacgggtg ctggccgcag tatttcccgc tccgccgcgg ctaccactcg
 540
 cacatcacct acaacgacga cgccatgggt aatgtgctcg acctgctgct ggacgtgtcg
 600
 ctgggagagg agccgttcga ttttgtggac gaggatcgcc gccagcgggc cgcgaccgcc
 660
 gtggagcggg ggatcgaatg catcctccgc acccaaattc ggcaggagga ccaaccacc
 720
 ggctggtgcg cgcagtatga cccgaaaacc ttggccccgg cgtggggacg ggctacgag
 780
 ccgccgtcga tttccggagc cgagaccgtc ggctggcgcg ggtttctgat gcggctggag
 840
 tcgccatcgc cggaagccgt cgaagccatc gagggcgcca tcgcctggct cgacacgggtg
 900
 ggcatcgagg aattgctct cgaatggttc accaacagcg agggcaagcg tgaccggcgc
 960
 gtggtcgagg acgcttccgt gggcaccctt tgggcgcgct ttacgaact cgaaacgaac
 1020
 cgcccttgt tcgtggaccg cgacggggtg ctccgctacg acttcgcgga actgacggcg
 1080
 gagcgccgcc aaggttacag ctactacggc acttggccgg cgccattgct ggccacggaa
 1140
 tatccgcgct ggcgaggat gaacgagtc gccctgctcg agtcgtcctt catctcgcat
 1200
 tga
 1203

<210> 106
 <211> 400
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(43)
 <221> DOMAIN
 <222> (44)...(400)
 <223> Catalytic domain

<400> 106

Met	Gln	Phe	Ile	Glu	Thr	Gln	Gln	Leu	Gly	Thr	Ala	Ala	Lys	Pro	Val
1				5					10					15	
Ala	Gly	Arg	Gly	Gly	Asp	Arg	Arg	Phe	Pro	Arg	Val	Met	Pro	Ala	Val
			20					25					30		
Cys	Ala	Gly	Leu	Ala	Leu	Ala	Val	Ser	Ser	Ala	Glu	Pro	Val	Arg	Ala
		35					40					45			
Gln	Gly	Ala	Asp	Ala	Asp	Ala	Asp	Gly	Pro	Leu	Pro	Arg	Trp	Asn	Arg
	50					55					60				
Arg	Leu	Val	Asp	Arg	Pro	Glu	Asp	Trp	Phe	Ala	Ser	Asp	Glu	Gly	Gln
65					70				75					80	
Arg	Val	Ala	Ala	Asn	Val	Leu	Arg	Tyr	Gln	Ser	Ala	Glu	Gly	Ala	Trp
				85					90					95	
Pro	Lys	Asn	Thr	Asn	Leu	Ala	Ala	Thr	Pro	Leu	Arg	Pro	Glu	Asp	Ile
			100					105					110		
Pro	Ser	Ser	Thr	Ser	Gly	Val	Ala	Asn	Thr	Ile	Asp	Asn	Glu	Ala	Thr
		115				120						125			
Thr	Val	Pro	Ile	Arg	Phe	Leu	Ala	Arg	Phe	Ala	Gln	Ile	Asn	Glu	Asp
	130					135					140				
Thr	Ala	Ser	Arg	Glu	Ala	Val	Gln	Arg	Gly	Leu	Asp	Tyr	Leu	Leu	Lys
145					150					155					160
Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Phe	Pro	Leu	Arg	Arg
				165					170					175	
Gly	Tyr	His	Ser	His	Ile	Thr	Tyr	Asn	Asp	Asp	Ala	Met	Val	Asn	Val
			180					185					190		
Leu	Asp	Leu	Leu	Leu	Asp	Val	Ser	Leu	Gly	Glu	Glu	Pro	Phe	Asp	Phe
	195					200						205			
Val	Asp	Glu	Asp	Arg	Arg	Gln	Arg	Ala	Ala	Thr	Ala	Val	Glu	Arg	Gly
	210					215					220				
Ile	Glu	Cys	Ile	Leu	Arg	Thr	Gln	Ile	Arg	Gln	Glu	Asp	Gln	Pro	Thr
225					230					235					240
Gly	Trp	Cys	Ala	Gln	Tyr	Asp	Pro	Glu	Thr	Leu	Ala	Pro	Ala	Trp	Gly
				245					250					255	
Arg	Ala	Tyr	Glu	Pro	Pro	Ser	Ile	Ser	Gly	Ala	Glu	Thr	Val	Gly	Val
			260					265					270		
Ala	Arg	Phe	Leu	Met	Arg	Leu	Glu	Ser	Pro	Ser	Pro	Glu	Ala	Val	Glu
		275				280						285			
Ala	Ile	Glu	Gly	Ala	Ile	Ala	Trp	Leu	Asp	Thr	Val	Gly	Ile	Glu	Glu
	290					295					300				
Leu	Arg	Leu	Glu	Trp	Phe	Thr	Asn	Ser	Glu	Gly	Lys	Arg	Asp	Arg	Arg
305					310					315					320
Val	Val	Glu	Asp	Ala	Ser	Val	Gly	Thr	Leu	Trp	Ala	Arg	Phe	Tyr	Glu
				325					330					335	
Leu	Glu	Thr	Asn	Arg	Pro	Leu	Phe	Val	Asp	Arg	Asp	Gly	Val	Leu	Arg
			340					345					350		
Tyr	Asp	Phe	Ala	Glu	Leu	Thr	Ala	Glu	Arg	Arg	Gln	Gly	Tyr	Ser	Tyr
		355					360					365			
Tyr	Gly	Thr	Trp	Pro	Ala	Pro	Leu	Leu	Ala	Thr	Glu	Tyr	Pro	Arg	Trp
	370					375					380				
Arg	Arg	Met	Asn	Glu	Ser	Ala	Leu	Leu	Glu	Ser	Ser	Phe	Ile	Ser	His
385					390					395					400

<210> 107
 <211> 1074
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 107
 atgacgctac ccgttggtttc cctgcgcgta ctgctggcgc tgctggccac gtcgccggtc

60
 gcctgcgcgg gcgctgcggc acccgcgact gcgaccgatc cggtcgcgga gaacatgctg
 120
 cttctgcaga ccgcctccgg cggctggtcc aagcactacc gcgagaagaa ggtcgactac
 180
 gcgcgcgact acgacgccgc cgagcgcgcc gcgctgcgcg cgcccgaccg gcatgacgat
 240
 gccacgatcg acaacaaggc caccgaccacc gagatcgcat acctggtgca ggcacatgcc
 300
 aggacgggca atccggccta cctcgacggc gcgcgccgcg gcgtcgagta cctgctgcgc
 360
 gcgcagtagc cgaacggcgg ctggccgcag ttctaccccc accattcgctc ctaccggcac
 420
 cagatcacgc tcaacgacga tgcgatggcg cacgccatca ccgtgctgca ggacatcgcc
 480
 gcgggccgca acggcatgca ggtgctggcg ccggagttcg gcgtccgcgc cgccgcggcc
 540
 gcgcagcgcg gcatcggaac cctgctcgag ttgcaggtgc ggatcgacgg ggtgccgacg
 600
 atctgggccg cgagtagcga cgagaccacc ctgcaaccgg ccaaggcccc tgcgtacgag
 660
 ttgccctcgc tggccgtggc cgaatcggtg ggcgtgatgc gcctgctgat gcgccagccg
 720
 gggcctgatg cgcgcacgat cgccgcgatc gaggcggcgg cggactggct ggaggcgcac
 780
 cgctgccggg acctcgccct ggaacgcacg gaagcccccg ccgaggaaac cggcaaggac
 840
 gtccgcgtcg tggccagacc gggcgcgtcg ttgtggggcg gcttctacga cctcgagcgg
 900
 caggtgccgc tggtcgtcga tcgcaacagc cgtccggttc cattcgccga gttcccaac
 960
 gagcgtcgta ccggctatgg ctggtatggc acctggccgg aaaagctgct ggcacaggaa
 1020
 ctcccgcgct ggcgcaaggc ccatgcggcc agcgcggggc ctccggcccc ttga
 1074

<210> 108
 <211> 357
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(31)

<221> DOMAIN
 <222> (32)...(357)
 <223> Catalytic domain

<400> 108
 Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
 1 5 10 15
 Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
 20 25 30
 Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
 35 40 45
 Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
 50 55 60
 Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp

65					70					75				80	
Ala	Thr	Ile	Asp	Asn	Lys	Ala	Thr	Thr	Thr	Glu	Ile	Ala	Tyr	Leu	Val
				85					90					95	
Gln	Ala	His	Ala	Arg	Thr	Gly	Asn	Pro	Ala	Tyr	Leu	Asp	Gly	Ala	Arg
			100					105					110		
Arg	Gly	Val	Glu	Tyr	Leu	Leu	Arg	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp
		115					120					125			
Pro	Gln	Phe	Tyr	Pro	Asp	His	Ser	Ser	Tyr	Arg	His	Gln	Ile	Thr	Leu
	130					135						140			
Asn	Asp	Asp	Ala	Met	Val	His	Ala	Ile	Thr	Val	Leu	Gln	Asp	Ile	Ala
145					150					155				160	
Ala	Gly	Arg	Asn	Gly	Met	Gln	Val	Leu	Ala	Pro	Glu	Phe	Gly	Val	Arg
			165						170					175	
Ala	Ala	Ala	Ala	Ala	Gln	Arg	Gly	Ile	Gly	Asn	Leu	Leu	Glu	Leu	Gln
			180						185					190	
Val	Arg	Ile	Asp	Gly	Val	Pro	Thr	Ile	Trp	Ala	Ala	Gln	Tyr	Asp	Glu
		195					200					205			
Thr	Thr	Leu	Gln	Pro	Ala	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Ser	Leu
	210					215					220				
Ala	Val	Ala	Glu	Ser	Val	Gly	Val	Met	Arg	Leu	Leu	Met	Arg	Gln	Pro
225					230					235					240
Gly	Pro	Asp	Ala	Arg	Thr	Ile	Ala	Ala	Ile	Glu	Ala	Ala	Ala	Asp	Trp
			245						250					255	
Leu	Glu	Ala	His	Arg	Leu	Pro	Asp	Leu	Ala	Leu	Glu	Arg	Ile	Glu	Ala
		260						265					270		
Pro	Ala	Glu	Glu	Thr	Gly	Lys	Asp	Val	Arg	Val	Val	Ala	Arg	Pro	Gly
		275					280					285			
Ala	Ser	Leu	Trp	Ala	Arg	Phe	Tyr	Asp	Leu	Glu	Arg	Gln	Val	Pro	Leu
	290					295					300				
Phe	Val	Asp	Arg	Asn	Ser	Arg	Pro	Val	Pro	Phe	Ala	Glu	Leu	Pro	Asn
305					310					315					320
Glu	Arg	Arg	Thr	Gly	Tyr	Gly	Trp	Tyr	Gly	Thr	Trp	Pro	Glu	Lys	Leu
			325						330					335	
Leu	Ala	Gln	Glu	Leu	Pro	Arg	Trp	Arg	Lys	Val	His	Ala	Ala	Ser	Ala
		340						345					350		
Gly	Ala	Pro	Ala	Arg											
		355													

<210> 109
 <211> 1422
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 109
 atgacgacac gacgcgaatt catcaaaggc tttctactta ccggagcagc cgtggccgctc
 60
 gctccgcggtt tgcttgcggt cgccgcggag gcaagtccgt gggaaacgat gatgccttcg
 120
 atcctcgcac gcatcagacc acctcgtttt ccgaaacgca ccttctatct caatcgattc
 180
 ggcgccaagg gtgatggagt cacagactgc accgcggctt ttcacgcgc gatcgatgaa
 240
 tgcaccaaag ccggcggtgg gaaagtcgtc gtgccggcgg gcacttatct caccggcgcg
 300
 attcatttga agagcaacgt caacctcgaa gtctcggaag gcgcgacgat caagttcagt
 360
 caggacccga aacactacct gcctgtgtgc ttctcgcggt gggaaggtgt cgaagtcttc
 420

aactactcgc ctttcattta cgcgttcgaa cagcgaaaca tcgcatcac cggcaaaggc
480
acgctcgacg gacagagtga ttcggaacac tgggtggccgt ggaacggccg tccgcagtac
540
ggatggaaaag aagggatgaa acagcagcgt cccgatcgca acgcgttggt cacaatggcg
600
gagaaaggcg tgccggtgcg cgagcgcac tttggcgaag gtcattattt gagggccgag
660
ttcattcagc cgtaccgctg ccagaacgtg ctgatccagg gctgacgat tcggaactcg
720
ccgatgtggg agattcatcc ggtgttgtgc cgtaacgtga ctattcacga cgtgcacatc
780
gatagtcagt gaccaaaca cgacggctgc aatcccgaat cgtgcagcga cgtgttgatt
840
aaggatagct acttcgatac cggcgacgac tgcacgcga tcaaactcgg acgcaacgcc
900
gacgggcccgc ggcttaaagc gccgactgag aacatcatcg ttcaaggatg tcgcatgaaa
960
gacggccacg gtggaatcac ggtcggcagc gagatctcgg gcggcgtgcg aaacctgttt
1020
gccgagaatt gccggctcga cagtccaaac ctcgatcacg ccctgcgcgt gaagaacaat
1080
gccatgcgcg gcggattact cgagaacttc cacttccgta acatcgaagt cgggcaggcg
1140
gcccattgccg tgattacgat cgacttcaac tacgaagagg gcgcgaaagg gtcgttcacg
1200
ccggtcgttc gcgattacac ggtcgcgcgt ttgcgcagca cgaagagcaa gcacgcactc
1260
gacgtccagg gtctgcccgg cgcgccggtc atcaacctgc gattgacgaa ctgcacattc
1320
aacgatgtgc agcaaccgaa cattctcaag aacgtcgaac aatcaacctt tgaaaacgtc
1380
acgattaacg gaaagacgat cacacaaaca ggatccaaag aa
1422

<210> 110
<211> 474
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (28)...(308)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (309)...(637)
<223> Catalytic domain

<400> 110
Met Thr Thr Arg Arg Glu Phe Ile Lys Gly Phe Leu Leu Thr Gly Ala
1 5 10 15
Ala Val Ala Val Ala Pro Arg Leu Leu Ala Phe Ala Ala Glu Ala Ser
20 25 30
Pro Trp Glu Thr Met Met Pro Ser Ile Leu Ala Arg Ile Arg Pro Pro
35 40 45

Arg	Phe	Pro	Lys	Arg	Thr	Phe	Tyr	Leu	Asn	Arg	Phe	Gly	Ala	Lys	Gly
50						55					60				
Asp	Gly	Val	Thr	Asp	Cys	Thr	Ala	Ala	Phe	His	Arg	Ala	Ile	Asp	Glu
65					70					75					80
Cys	Thr	Lys	Ala	Gly	Gly	Gly	Lys	Val	Val	Val	Pro	Ala	Gly	Thr	Tyr
				85					90					95	
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Val	Ser
			100					105					110		
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asp	Pro	Lys	His	Tyr	Leu	Pro
		115					120					125			
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
		130				135					140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Arg	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
145					150					155					160
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Ser	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
				165					170					175	
Arg	Pro	Gln	Tyr	Gly	Trp	Lys	Glu	Gly	Met	Lys	Gln	Gln	Arg	Pro	Asp
			180					185					190		
Arg	Asn	Ala	Leu	Phe	Thr	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Arg	Glu
		195					200					205			
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
	210					215					220				
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Gln	Gly	Val	Thr	Ile	Arg	Asn	Ser
225					230					235					240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Thr	Ile	His
				245					250					255	
Asp	Val	His	Ile	Asp	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
			260					265					270		
Glu	Ser	Cys	Ser	Asp	Val	Leu	Ile	Lys	Asp	Ser	Tyr	Phe	Asp	Thr	Gly
		275					280					285			
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
	290					295					300				
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Gln	Gly	Cys	Arg	Met	Lys
305					310					315					320
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
				325					330					335	
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
			340					345					350		
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
		355					360					365			
Asn	Phe	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala	Val
						375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385					390					395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Arg	Leu	Arg	Ser	Thr	Lys	Ser
				405					410					415	
Lys	His	Ala	Leu	Asp	Val	Gln	Gly	Leu	Pro	Gly	Ala	Pro	Val	Ile	Asn
			420					425					430		
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asn	Asp	Val	Gln	Gln	Pro	Asn	Ile
		435					440					445			
Leu	Lys	Asn	Val	Glu	Gln	Ser	Thr	Phe	Glu	Asn	Val	Thr	Ile	Asn	Gly
	450					455					460				
Lys	Thr	Ile	Thr	Gln	Thr	Gly	Ser	Lys	Glu						
465					470										

<210> 111
 <211> 1440
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 111

atgcaaaatc gtcgagaatt tttacaactt ttatttgccg gtgccggtgc cggacttggt
60
ttgccgcaga tttcttttcg gcagactaaa caagccgacg cctggacgac cgagtatccg
120
aagatttttag ccagaatcaa accgccgaaa tttcgcaaaa aagattttcc gatcaccaaa
180
tatggagccg ttgcgggacg gaaaaccctg gcgaccgaaa gcatcaaaaa agccatcgaa
240
gcgtgcgcca aatcgggacg cgggacgctc gtcgtgcccc agggagaatt tttgaccggc
300
gcgattcatt tgaaatcaaa cgtcaatctg cacatcacga aaggcgcgac cgtcaaattt
360
tccaccaacc cgaaagatta tctgccgatc gttcacacgc gctgggaagg gatggaattg
420
atgcatattt cgcctttaat ttatgcctac gagcaaacca acatcgccgt caccggcgag
480
ggaacgctcg acgggcaggg caaggctttt ttctggaaat ggcacggaac cccgcgctac
540
ggcggaatc cggtatgat cagccagcgt ccggcgcgcg cccggctgta tgaaatgatg
600
gaaaaaggcg tgcctgtggc ggagcggatt ttcggcgaaa ctcagtatct tcgcccgcag
660
tttatccagc cctataaatg caaaaatggt ttgatcgaag gcgttaaaat catcgattcg
720
ccgatgtggg aagttcaccc cgttttgtgc gaaaacgtga cgatccgaaa acttcatatt
780
tctaccacg gaccgaacaa cgacgggtgc gatccggaac gctgcaagga cgttttgatc
840
gaagactgct atttcgacac cggcgacgat tgcattgcca tcaaggcggg gcgcaatgaa
900
gacgggacg gcatcaatgt tccgaccgaa aacgtcgtcg tgcgcgggtg cgtgatgaag
960
gacggtcacg gcggaatcac catcggaagc gagatttccg gcggcgtgcg aaatgttttc
1020
gcggaaaaca accggctcga cagcgcggtt ttgtggactg cgctgagagt gaaaaacaac
1080
gcttcgcgcg gcggaaaact ggagaatttt tacttccgcg atatcaccgt cgggcaggtc
1140
tcgcgcgcg tgcgcgaaat agattttaat tacgaggaag gcgctaaagg aaaacacacg
1200
ccggtcgttc gcaattacgt ggtcgaaaat ctaacctgca ataaaggcaa tcgagcggtc
1260
gatctgcagg gcttgacaaa cgccccgatt tacgacatca cgatgaaaaa ctgtacgttt
1320
aacgtgggtc aaaaagccgag cgtcgtgaaa aacgtcaaag gcgtcaaaact ggaaaacgtg
1380
aagattaacg gcaaagtcgt cgagagtctg gaaaatgctg caacgacgac taaaaataa
1440

<210> 112

<211> 479

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(27)

<221> DOMAIN

<222> (82)...(461)

<223> Catalytic domain

<400> 112

Met	Gln	Asn	Arg	Arg	Glu	Phe	Leu	Gln	Leu	Leu	Phe	Ala	Gly	Ala	Gly
1				5					10					15	
Ala	Gly	Leu	Val	Leu	Pro	Gln	Ile	Ser	Phe	Gly	Gln	Thr	Lys	Gln	Ala
			20					25					30		
Asp	Ala	Trp	Thr	Thr	Glu	Tyr	Pro	Lys	Ile	Leu	Ala	Arg	Ile	Lys	Pro
		35					40					45			
Pro	Lys	Phe	Arg	Lys	Lys	Asp	Phe	Pro	Ile	Thr	Lys	Tyr	Gly	Ala	Val
	50					55					60				
Ala	Asp	Gly	Lys	Thr	Leu	Ala	Thr	Glu	Ser	Ile	Lys	Lys	Ala	Ile	Glu
65					70					75					80
Ala	Cys	Ala	Lys	Ser	Gly	Gly	Gly	Arg	Val	Val	Val	Pro	Gln	Gly	Glu
				85					90					95	
Phe	Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	His	Ile
			100					105					110		
Thr	Lys	Gly	Ala	Thr	Val	Lys	Phe	Ser	Thr	Asn	Pro	Lys	Asp	Tyr	Leu
		115						120					125		
Pro	Ile	Val	His	Thr	Arg	Trp	Glu	Gly	Met	Glu	Leu	Met	His	Ile	Ser
	130					135					140				
Pro	Leu	Ile	Tyr	Ala	Tyr	Glu	Gln	Thr	Asn	Ile	Ala	Val	Thr	Gly	Glu
145					150					155					160
Gly	Thr	Leu	Asp	Gly	Gln	Gly	Lys	Ala	Phe	Phe	Trp	Lys	Trp	His	Gly
				165					170					175	
Asn	Pro	Arg	Tyr	Gly	Gly	Asn	Pro	Asp	Val	Ile	Ser	Gln	Arg	Pro	Ala
			180					185					190		
Arg	Ala	Arg	Leu	Tyr	Glu	Met	Met	Glu	Lys	Gly	Val	Pro	Val	Ala	Glu
		195					200					205			
Arg	Ile	Phe	Gly	Glu	Thr	Gln	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
	210					215					220				
Tyr	Lys	Cys	Lys	Asn	Val	Leu	Ile	Glu	Gly	Val	Lys	Ile	Ile	Asp	Ser
225					230					235					240
Pro	Met	Trp	Glu	Val	His	Pro	Val	Leu	Cys	Glu	Asn	Val	Thr	Ile	Arg
				245					250					255	
Lys	Leu	His	Ile	Ser	Thr	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asp	Pro
		260						265					270		
Glu	Ser	Cys	Lys	Asp	Val	Leu	Ile	Glu	Asp	Cys	Tyr	Phe	Asp	Thr	Gly
		275					280					285			
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ala	Gly	Arg	Asn	Glu	Asp	Gly	Arg	Arg
	290					295					300				
Ile	Asn	Val	Pro	Thr	Glu	Asn	Val	Val	Val	Arg	Gly	Cys	Val	Met	Lys
305					310					315					320
Asp	Gly	His	Gly	Gly	Ile	Thr	Ile	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
			325						330					335	
Arg	Asn	Val	Phe	Ala	Glu	Asn	Asn	Arg	Leu	Asp	Ser	Ala	Asp	Leu	Trp
			340					345					350		
Thr	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Ser	Arg	Gly	Gly	Lys	Leu	Glu
		355					360					365			
Asn	Phe	Tyr	Phe	Arg	Asp	Ile	Thr	Val	Gly	Gln	Val	Ser	Arg	Ala	Val
	370					375					380				
Val	Glu	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Lys	His	Thr
385					390					395					400
Pro	Val	Val	Arg	Asn	Tyr	Val	Val	Glu	Asn	Leu	Thr	Cys	Asn	Lys	Gly
				405					410					415	
Asn	Arg	Ala	Val	Asp	Leu	Gln	Gly	Leu	Asp	Asn	Ala	Pro	Ile	Tyr	Asp
			420					425					430		

Ile	Thr	Met	Lys	Asn	Cys	Thr	Phe	Asn	Val	Val	Glu	Lys	Pro	Ser	Val
		435					440					445			
Val	Lys	Asn	Val	Lys	Gly	Val	Lys	Leu	Glu	Asn	Val	Lys	Ile	Asn	Gly
	450				455						460				
Lys	Val	Val	Glu	Ser	Leu	Glu	Asn	Ala	Ala	Thr	Thr	Ala	Lys	Lys	
465					470					475					

<210> 113
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 113
 atgaagatat ttttaacaat attgctctcg gcattattca gcatttcaaa tgcacaggtg
 60
 ctatcggatc ctgttgcgga tcgtatgacc agctaccaac ttaaaaacgg aggctggccg
 120
 aagcacttgg ccgataaatc tggtgttaac tattcaaaac ctctctcacc tgctttgcaa
 180
 aaagtcacgc atcaatcgac cgaaaagtct gcgacaattg ataataatgc aaccacacgt
 240
 gagataaacc atcttctcct cgcttattcc aaaaccaaca atgacaagta tcttcaagcg
 300
 gcgacaaaag gtgttgagta tatcctgagt gctcaaaatg acaaaggagg atggcctcaa
 360
 tattatccag acagtagctc atatcgtggt cagatcacct acaatgacgg cgcgatgatt
 420
 aatgtattgg aaattttact ttccatatca acaaaacaag agccctatgc tgttctaacg
 480
 aataaattta acgaaagaat agaaagggcc ttaacacgag ggattcactg catcttacia
 540
 acccaggtta aacaaggaga taaactaacc atctggggccg cacagtacga tcagaaaaca
 600
 atggaacctg ctcaagccag actgtttgaa ccggtagcgt tagcgacagc ggaatcggcg
 660
 ggcattctcc gctttttaat gcgtcttgac catcctactc ccgaaataaa aaatgcaatc
 720
 aaccacgctg tagaatggtt ttctcccat aaagaggtag gctatgatta cgttaaaacg
 780
 gaaaaaacg gaaaactttt gcgggatttg gtttcttcgc cggcctctac cgtatgggca
 840
 agattttatg acatcaggac gaatcaacct atctttggtg atcgcgataa tacgataaag
 900
 tattcgctga atgaaataag cgaggaacga caaatggct actcttggtg tggttaactgg
 960
 ccagaaaaga taattacaaa agaatatgaa aaatggctta agaaggtaaa tgaataa
 1017

<210> 114
 <211> 338
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN
 <222> (19)...(388)
 <223> Catalytic domain

<400> 114

Met	Lys	Ile	Phe	Leu	Thr	Ile	Leu	Leu	Ser	Ala	Leu	Phe	Ser	Ile	Ser
1				5					10					15	
Asn	Ala	Gln	Val	Leu	Ser	Asp	Pro	Val	Ala	Asp	Arg	Met	Thr	Ser	Tyr
			20					25					30		
Gln	Leu	Lys	Asn	Gly	Gly	Trp	Pro	Lys	His	Leu	Ala	Asp	Lys	Ser	Val
		35					40					45			
Val	Asn	Tyr	Ser	Lys	Pro	Leu	Ser	Pro	Ala	Leu	Gln	Lys	Val	Ile	Asp
	50					55					60				
Gln	Ser	Thr	Glu	Lys	Ser	Ala	Thr	Ile	Asp	Asn	Asn	Ala	Thr	Thr	Arg
65					70					75					80
Glu	Ile	Asn	His	Leu	Leu	Leu	Ala	Tyr	Ser	Lys	Thr	Asn	Asn	Asp	Lys
			85						90					95	
Tyr	Leu	Gln	Ala	Ala	Thr	Lys	Gly	Val	Glu	Tyr	Ile	Leu	Ser	Ala	Gln
			100					105						110	
Asn	Asp	Lys	Gly	Gly	Trp	Pro	Gln	Tyr	Tyr	Pro	Asp	Ser	Ser	Ser	Tyr
		115					120					125			
Arg	Gly	Gln	Ile	Thr	Tyr	Asn	Asp	Gly	Ala	Met	Ile	Asn	Val	Leu	Glu
	130					135					140				
Ile	Leu	Leu	Ser	Ile	Ser	Thr	Lys	Gln	Glu	Pro	Tyr	Ala	Val	Leu	Thr
145					150					155					160
Asn	Lys	Phe	Asn	Glu	Arg	Ile	Glu	Arg	Ala	Leu	Thr	Arg	Gly	Ile	His
			165						170					175	
Cys	Ile	Leu	Gln	Thr	Gln	Val	Lys	Gln	Gly	Asp	Lys	Leu	Thr	Ile	Trp
		180						185					190		
Ala	Ala	Gln	Tyr	Asp	Gln	Lys	Thr	Met	Glu	Pro	Ala	Gln	Ala	Arg	Leu
		195					200					205			
Phe	Glu	Pro	Val	Ala	Leu	Ala	Thr	Ala	Glu	Ser	Ala	Gly	Ile	Leu	Arg
	210					215					220				
Phe	Leu	Met	Arg	Leu	Asp	His	Pro	Thr	Pro	Glu	Ile	Lys	Asn	Ala	Ile
225					230					235					240
Asn	His	Ala	Val	Glu	Trp	Phe	Ser	Ser	His	Lys	Glu	Val	Gly	Tyr	Asp
			245						250					255	
Tyr	Val	Lys	Thr	Glu	Lys	Asn	Gly	Lys	Leu	Leu	Arg	Asp	Leu	Val	Ser
			260					265					270		
Ser	Pro	Ala	Ser	Thr	Val	Trp	Ala	Arg	Phe	Tyr	Asp	Ile	Arg	Thr	Asn
		275					280					285			
Gln	Pro	Ile	Phe	Gly	Asp	Arg	Asp	Asn	Thr	Ile	Lys	Tyr	Ser	Leu	Asn
	290					295					300				
Glu	Ile	Ser	Glu	Glu	Arg	Gln	Asn	Gly	Tyr	Ser	Trp	Tyr	Gly	Asn	Trp
305					310					315					320
Pro	Glu	Lys	Ile	Ile	Thr	Lys	Glu	Tyr	Glu	Lys	Trp	Leu	Lys	Lys	Val
				325					330					335	

Asn Glu

<210> 115
 <211> 996
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 115
 gtggccaagg cgatcggcgg tccgttgccg ccggcaccag ggcagggatc gccggtaacg

60
 tgggcgacga ttctccggca gccatcgccg tggtagcggt ccgcgagacgc gaaggcggtt
 120
 gccgaaaccg tgcgcgcgag ccagagagcc accggcggtt ggccgaagaa cacggattgg
 180
 acggcgctcc agagcgacgc tgagcggcag gcgctgcgaa atgcccgcgc cgagaccgat
 240
 tcgacgatcg acaatggcgc cacggtcacc gagcttcgct ttctcaccgc cgtgtatgtc
 300
 gccacgcgcg acgagctttt acgggagggc gtgcttcgcg gcctcgacta cctgctggcg
 360
 tcgcagtaca gcaacggcgc ctggccacaa tactttccgt tgcggaccga ttactcgcgc
 420
 gacatcacgt tcaacgacga cgcgatgacc ggctgtgtgc tgctgtgtaa ggatgccgcg
 480
 gacgggtcag caggtttcga attcgtcgac aaggcgagac gtgaccgcgc tgccgcggcc
 540
 gtgacgcgcg ccacgcgggt gaccccgccg acgcagattc gggcaaacgc tacgtgacc
 600
 ggctgtgtgc agcagtacga cgcgcgcgcg ctgacgccgc cgcgcgggcg ctctacgag
 660
 catccgtcga ttgcgagccg cgagacggtc gggatcgcgc ggctgtgat gggcgtgccg
 720
 aatccgtcgc cagagatcgt ggctgccgtt gacgcggctg ccgcatggtt gggtaaatac
 780
 gaactgaagg gtgtgcccga ggcgacggcg ccaggacttt gggcgcgctt ctacgacatc
 840
 gctacgaatc ggccgatcta ttcggggcgc gacggcgctc tcaagtaccg gctcgacgag
 900
 atcgagctcg agcggcgcac aggctacagc tgggttggcc cgtacgccgc ggcatttctg
 960
 acgaccgaat atccgaaatg gcgggcggca cgatga
 996

<210> 116
 <211> 331
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(331)
 <223> Catalytic domain

<400> 116
 Met Ala Lys Ala Ile Gly Gly Pro Leu Pro Pro Ala Pro Gly Gln Gly
 1 5 10 15
 Ser Pro Val Thr Trp Ala Thr Ile Leu Arg Gln Pro Ser Pro Trp Tyr
 20 25 30
 Ala Ser Ala Asp Ala Lys Ala Val Ala Glu Thr Val Arg Ala Ser Gln
 35 40 45
 Arg Ala Thr Gly Gly Trp Pro Lys Asn Thr Asp Trp Thr Ala Leu Gln
 50 55 60
 Ser Asp Ala Glu Arg Gln Ala Leu Arg Asn Ala Arg Ala Glu Thr Asp
 65 70 75 80
 Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Glu Leu Arg Phe Leu Thr
 85 90 95
 Arg Val Tyr Val Ala Thr Arg Asp Glu Leu Leu Arg Glu Ala Val Leu
 100 105 110

Arg	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ser	Gln	Tyr	Ser	Asn	Gly	Gly	Trp
		115					120					125			
Pro	Gln	Tyr	Phe	Pro	Leu	Arg	Thr	Asp	Tyr	Ser	Arg	Asp	Ile	Thr	Phe
		130				135					140				
Asn	Asp	Asp	Ala	Met	Thr	Gly	Val	Val	Leu	Leu	Leu	Lys	Asp	Ala	Ala
145					150					155					160
Asp	Gly	Ser	Ala	Gly	Phe	Glu	Phe	Val	Asp	Lys	Ala	Arg	Arg	Asp	Arg
			165						170					175	
Ala	Ala	Ala	Ala	Val	Thr	Arg	Ala	Ile	Ala	Val	Ile	Leu	Arg	Thr	Gln
			180					185					190		
Ile	Arg	Val	Asn	Gly	Thr	Leu	Thr	Gly	Trp	Cys	Gln	Gln	Tyr	Asp	Ala
		195					200					205			
Asp	Ala	Leu	Thr	Pro	Ala	Arg	Gly	Arg	Ser	Tyr	Glu	His	Pro	Ser	Ile
	210					215					220				
Ala	Ser	Arg	Glu	Thr	Val	Gly	Ile	Ala	Arg	Leu	Leu	Met	Gly	Val	Pro
225					230					235					240
Asn	Pro	Ser	Pro	Glu	Ile	Val	Ala	Ala	Val	Asp	Ala	Ala	Ala	Ala	Trp
				245					250					255	
Leu	Gly	Lys	Ser	Glu	Leu	Lys	Gly	Val	Pro	Glu	Ala	Thr	Ala	Pro	Gly
			260					265					270		
Leu	Trp	Ala	Arg	Phe	Tyr	Asp	Ile	Ala	Thr	Asn	Arg	Pro	Ile	Tyr	Ser
		275					280					285			
Gly	Arg	Asp	Gly	Val	Ile	Lys	Tyr	Arg	Leu	Asp	Glu	Ile	Glu	Leu	Glu
	290					295					300				
Arg	Arg	Thr	Gly	Tyr	Ser	Trp	Val	Gly	Pro	Tyr	Ala	Ala	Ala	Phe	Leu
305					310					315					320
Thr	Thr	Glu	Tyr	Pro	Lys	Trp	Arg	Ala	Ala	Arg					
				325					330						

<210> 117
 <211> 1725
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 117
 atgaagaatt ttgggtttgg taactacaag tttttttagt cggaatgtc tgtcgcgtct
 60
 ttttcgtatg cggcaagcta tacacccccg tcaacagcag tttcgaaaat caacagctat
 120
 cgaggctatt cggagctgac ttcagctgca tccggcatgg atatcgacca gtacacctac
 180
 aacatgacca cttggcaaat cgaaaacggc ggtttttaca aagccatggc cgacaagtat
 240
 aaaagcgcgt atggcggcgg tcaaaaatcc gaatggcaag ctaaaggcgg tggcgacctc
 300
 ggactatag acaacaacgc caccatccag gaaatgcgtt tgctcgccgt gcgttacaaa
 360
 gaaacgacga acaacaatta caaatccgca tttaagacaa gtttcaacaa ggcggtcaat
 420
 tttcttttga ccatgcagcg ctccaaaggc ggactcccac aagtttggcc caaacgcggc
 480
 aactattctg accaaatcac gctaaatgac aacgccatga tccgcgccat ggtcacgatg
 540
 atggatatcg ccaacaagac gagtccattt gattcggata tcatcgacga cgccaccgcg
 600
 agcaaaatga aatcgggtctt cgacaaagcg gtcgattact tgctcaaggc gcaaatcgtg
 660
 aacgacggaa aggtcacggt atggtgcgcc cagcacgaca ccaacagcct cgccccgta

720
 ggcgacgag cctacgaact cccgagcaaa tccggcaacg aatccatggg cgttggtgtg
 780
 tttttgatga actggccaga ccaaaacgaa gcaatccaga aggcggtcaa aggcgcaatc
 840
 gcttggtaca aaaagaataa actaaaagac aaggcggtta gcaagaccgc aggcgttgtg
 900
 gacaaggcgg gttcatcgct gtggttccgc ttttacgaag tcaacaacga caactacttt
 960
 ttctgcgacc gcgatggtgc tagcaccaag acgcaggact tcatgaaaat cagcgaagaa
 1020
 cgtcgcaagg gctaccagtg ggcaggcgat tacggctctg caattctagg caccgaaaat
 1080
 gcataccttg aagcactcgc caagatggac gacaactatg ttccacctcc gccagcacca
 1140
 gctatgtgcg gaaacgacac ttgcaaaacg tacatcgatg gcgttgactt tattgacatt
 1200
 caaggcgta aggaacaac caacacggga ttcgttggcg aaggttacgc caacgttgac
 1260
 aactccaccg gaagctatgt gacctacggc gtcaccgcat tcaaggaagg caaatacact
 1320
 ttgttcatca gctttgcaaa cggcggtggt tccgcacgcg gttacagcgt ttctgcagga
 1380
 gacaagacgt tacttgaga cggcagcatg gaatctacag ccgcatggac cacttgga
 1440
 atgcaatcca tcgaaatcga attgccaatg ggctatagcg aactcaagtt cacaagcctt
 1500
 tcgaaagacg gtatggcgaa catcgattac atcggctgga tgaacgatga tttgaaagt
 1560
 ggcgaaagtg aagtaccacg ctcatccatt gaagcaatac gcgccatccg caaagcccag
 1620
 caggacaacc gctactttgt ggactttggc ggcaacaata atagcgcagg ggcttacttt
 1680
 aagcgtggca tcaacacggt ccgcgtgaat gggaagatga ggtaa
 1725

<210> 118
 <211> 574
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(24)

<221> DOMAIN
 <222> (25)...(574)
 <223> Catalytic domain

<400> 118
 Met Lys Asn Phe Gly Phe Gly Asn Tyr Lys Phe Phe Val Ala Ala Met
 1 5 10 15
 Ser Val Ala Ser Phe Ser Tyr Ala Ala Ser Tyr Thr Pro Pro Ser Thr
 20 25 30
 Ala Val Ser Lys Ile Asn Ser Tyr Arg Gly Tyr Ser Glu Leu Thr Ser
 35 40 45
 Ala Ala Ser Gly Met Asp Ile Asp Gln Tyr Thr Tyr Asn Met Thr Thr
 50 55 60
 Trp Gln Ile Ala Asn Gly Gly Phe Tyr Lys Ala Met Ala Asp Lys Tyr

65					70					75					80
Lys	Ser	Ala	Tyr	Gly 85	Gly	Gly	Gln	Lys	Ser 90	Glu	Trp	Gln	Ala	Lys 95	Gly
Gly	Gly	Asp	Leu 100	Gly	Thr	Ile	Asp	Asn 105	Asn	Ala	Thr	Ile	Gln 110	Glu	Met
Arg	Leu	Leu 115	Ala	Val	Arg	Tyr	Lys 120	Glu	Thr	Thr	Asn 125	Asn	Asn	Tyr	Lys
Ser	Ala	Phe 130	Lys	Thr	Ser	Phe 135	Asn	Lys	Ala	Val	Asn 140	Phe	Leu	Leu	Thr
Met 145	Gln	Arg	Ser	Lys	Gly 150	Gly	Leu	Pro	Gln	Val 155	Trp	Pro	Lys	Arg	Gly 160
Asn	Tyr	Ser	Asp	Gln 165	Ile	Thr	Leu	Asn	Asp 170	Asn	Ala	Met	Ile	Arg 175	Ala
Met	Val	Thr	Met 180	Met	Asp	Ile	Ala	Asn 185	Lys	Thr	Ser	Pro	Phe 190	Asp	Ser
Asp	Ile	Ile 195	Asp	Asp	Ala	Thr	Arg 200	Ser	Lys	Met	Lys	Ser 205	Ala	Leu	Asp
Lys	Ala	Val 210	Asp	Tyr	Leu	Leu 215	Lys	Ala	Gln	Ile	Val 220	Asn	Asp	Gly	Lys
Val 225	Thr	Val	Trp	Cys	Ala 230	Gln	His	Asp	Thr	Asn 235	Ser	Leu	Ala	Pro	Val 240
Gly	Ala	Arg	Ala	Tyr 245	Glu	Leu	Pro	Ser	Lys 250	Ser	Gly	Asn	Glu	Ser 255	Met
Gly	Val	Val	Trp 260	Phe	Leu	Met	Asn	Trp 265	Pro	Asp	Gln	Asn	Glu 270	Ala	Ile
Gln	Lys	Ala 275	Val	Lys	Gly	Ala	Ile 280	Ala	Trp	Tyr	Lys	Lys 285	Asn	Lys	Leu
Lys	Asp	Lys 290	Ala	Phe	Ser	Lys 295	Thr	Ala	Gly	Val	Val 300	Asp	Lys	Ala	Gly
Ser 305	Ser	Leu	Trp	Phe	Arg 310	Phe	Tyr	Glu	Val	Asn 315	Asn	Asp	Asn	Tyr	Phe 320
Phe	Cys	Asp	Arg	Asp 325	Gly	Ala	Ser	Thr	Lys 330	Thr	Gln	Asp	Phe	Met 335	Lys
Ile	Ser	Glu	Glu 340	Arg	Arg	Lys	Gly	Tyr 345	Gln	Trp	Ala	Gly	Asp 350	Tyr	Gly
Ser	Ala	Ile 355	Leu	Gly	Thr	Glu	Asn 360	Ala	Tyr	Leu	Glu	Ala 365	Leu	Ala	Lys
Met	Asp	Asp 370	Asn	Tyr	Val	Pro 375	Pro	Pro	Pro	Ala	Pro 380	Ala	Met	Cys	Gly
Asn 385	Asp	Thr	Cys	Lys	Thr 390	Tyr	Ile	Asp	Gly	Val 395	Asp	Phe	Ile	Asp	Ile 400
Gln	Gly	Val	Lys	Glu 405	Thr	Thr	Asn	Thr	Gly 410	Phe	Val	Gly	Glu 415	Gly	Tyr
Ala	Asn	Val	Asp 420	Asn	Ser	Thr	Gly	Ser 425	Tyr	Val	Thr	Tyr	Gly 430	Val	Thr
Ala	Phe	Lys 435	Glu	Gly	Lys	Tyr	Thr 440	Leu	Phe	Ile	Ser	Phe 445	Ala	Asn	Gly
Gly	Gly	Ser 450	Ala	Arg	Gly	Tyr 455	Ser	Val	Ser	Ala	Gly 460	Asp	Lys	Thr	Leu
Leu 465	Ala	Asp	Gly	Ser	Met 470	Glu	Ser	Thr	Ala	Ala 475	Trp	Thr	Thr	Trp	Lys 480
Met	Gln	Ser	Ile	Glu 485	Ile	Glu	Leu	Pro	Met 490	Gly	Tyr	Ser	Glu	Leu 495	Lys
Phe	Thr	Ser	Leu 500	Ser	Lys	Asp	Gly	Met 505	Ala	Asn	Ile	Asp	Tyr 510	Ile	Gly
Trp	Met	Asn 515	Asp	Asp	Leu	Lys	Val 520	Gly	Glu	Val	Glu	Val 525	Pro	Arg	Ser
Ser	Ile	Glu 530	Ala	Ile	Arg	Ala 535	Ile	Arg	Lys	Ala	Gln 540	Gln	Asp	Asn	Arg
Tyr 545	Phe	Val	Asp	Phe	Gly 550	Asn	Asn	Asn	Ser 555	Ala	Gly	Ala	Tyr	Phe	560

Lys Arg Gly Ile Asn Thr Phe Arg Val Asn Gly Lys Met Arg
565 570

<210> 119
<211> 1848
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 119
gtgtcatggc aggaatccgg tgcggctatc accaacgcct ggaatgcaac gctcagtggc
60
tcaaaccctt acacagccgt atccgctggt tggaatggca cacttgcccc caatgcatcg
120
gccacttttg gtttccaggc aaacggttct gccggtgcac cttaaagtga tggcagcttg
180
tgcggcacca acacttcac aacaccggca tccagcagtg ttgccagctc ggttaaatac
240
agcgcgcccc tatcgtccag cagcagatca tccagttcaa tcgctatcac tagcagctct
300
ttagcgagaa gttctattgc ctccagcagc tcactagtta gtagctccag agcgagcagt
360
agtgcgcaa gcgttttctc ttttacgac caggaagagc aagcgggctt ctgtcgtgtt
420
gatggcattg cgacagaaa caccaacacc ggttttaccg gcaatggcta caccaatgcg
480
aacaacgcgc aaggcgcagc gattgaatgg gcagtcagcg cacctagcag tggccgttat
540
acagtagcct tccgcttcgc caatggcggc acagcagcgc gcaacggctc gttgttaac
600
aatggcggtg gcaatggtta ttacactgtg gagttacccc tgaccggcgc atgggcaacc
660
tggcaaatg ccagcgtgga aattgattta gtgcaaggca ataataat tttt aaactctcg
720
gcgttaaccg ctgacggttt ggccaatc gactcattaa aaatagacgg cgcgcaaacc
780
aaagcaggta cttgcagcac tacatcaagc agcagcgttg ccagcagctc gtcgtccgtt
840
aaatccagcg caagtcttc ttcgagttca tccaccgctg caaaaatact gacattagac
900
ggtaaccg cgcgcagctg gttcaacaaa tccaggacca agtggaatag cagccgcgcc
960
gatattgtgt tgtcttacca gcaatccaac ggcggttggc caaaaaacct ggattacaac
1020
tcagtgcg caggcaatgg cgggagcgac agcggcacca tcgacaatgg tgcaaccatt
1080
accgaaatgg tttacctcgc tgaaatttat aaaaacggcg gcaacaccaa atatcgcgat
1140
gcagtgcgca gagcagcaaa ctttttagtg agctcgcaat acagcacagg cgccttgcca
1200
caattttatc cggtgaaagg cggctatgcg gatcatgcga cctttaacga taacggcatg
1260
gcgtacgcgt tgacggtatt ggatttcgca gtaaacaac gcgcaccgtt tgataacgac
1320
attttctctg attctgatcg ggcgaaattc aaaaccgctg ttgcaaagg tgtggattac
1380
attttaaaag cgcagtggaa acaaaatgga aaactcactg catgggtgtgc acaacacgg
1440
gctacggatt accaaccgaa aaaagcgcgc gcttatgaat tggaatcatt gagtggtagc

1500
gagtcggtcg gcattctcgc cttcttgatg acccaaccac aaaccgcgca aatcgaagcg
1560
gcggtcaagg cgggtgtcaa ctggttcgcc agtccaaata cttatttggc taactacact
1620
tacgattcat caaaagcgtc taccaacccg attgtgtata aatccggaag cagaatgtgg
1680
tatcgcttct atgacctgaa caccaaccgt ggtttcttta gtgatcgca tggcagcaaa
1740
ttctatgata tcacccaaat gtcagaagag cgtcgcaccg gttatagctg ggggtggctct
1800
tacggtgaat ctattatttc cttcgcgcaa aaagtgggtt atctgtaa
1848

<210> 120
<211> 615
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> BINDING
<222> (1)...(61)
<223> Carbohydrate binding module

<221> BINDING
<222> (134)...(257)
<223> Carbohydrate binding module

<221> DOMAIN
<222> (258)...(615)
<223> Catalytic domain

<400> 120
Met Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn Ala
1 5 10 15
Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp Asn
20 25 30
Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala Asn
35 40 45
Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr Asn
50 55 60
Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys Ser
65 70 75 80
Ser Ala Pro Val Ser Ser Ser Arg Ser Ser Ser Ser Ile Ala Ile
85 90 95
Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser Leu
100 105 110
Val Ser Ser Ser Arg Ala Ser Ser Ser Ala Pro Ser Val Phe Ser Phe
115 120 125
Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile Ala
130 135 140
Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn Ala
145 150 155 160
Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro Ser
165 170 175
Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr Ala
180 185 190
Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly Asn Tyr
195 200 205

Thr	Val	Glu	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Ile	Ala
	210					215					220				
Ser	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu	Ser
225					230					235					240
Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile	Asp
				245					250					255	
Gly	Ala	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ser	Thr	Thr	Ser	Ser	Ser	Ser
			260					265					270		
Val	Ala	Ser	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ser	Ser	Ser
		275					280					285			
Ser	Ser	Ser	Thr	Ala	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala
	290					295					300				
Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg	Ala
305					310					315					320
Asp	Ile	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn
				325					330					335	
Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser	Gly
			340					345					350		
Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala	Glu
		355					360					365			
Ile	Tyr	Lys	Asn	Gly	Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg	Arg
	370					375					380				
Ala	Ala	Asn	Phe	Leu	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu	Pro
385					390					395					400
Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe	Asn
				405					410					415	
Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val	Asn
			420					425				430			
Lys	Arg	Ala	Pro	Phe	Asp	Asn	Asp	Ile	Phe	Ser	Asp	Ser	Asp	Arg	Ala
		435					440					445			
Lys	Phe	Lys	Thr	Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys	Ala
	450					455					460				
Gln	Trp	Lys	Gln	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys	Ala	Gln	His	Gly
465					470					475					480
Ala	Thr	Asp	Tyr	Gln	Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu	Ser
				485					490					495	
Leu	Ser	Gly	Ser	Glu	Ser	Val	Gly	Ile	Leu	Ala	Phe	Leu	Met	Thr	Gln
			500					505					510		
Pro	Gln	Thr	Ala	Gln	Ile	Glu	Ala	Ala	Val	Lys	Ala	Gly	Val	Asn	Trp
		515					520					525			
Phe	Ala	Ser	Pro	Asn	Thr	Tyr	Leu	Ala	Asn	Tyr	Thr	Tyr	Asp	Ser	Ser
	530					535					540				
Lys	Ala	Ser	Thr	Asn	Pro	Ile	Val	Tyr	Lys	Ser	Gly	Ser	Arg	Met	Trp
545					550					555					560
Tyr	Arg	Phe	Tyr	Asp	Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp	Arg
				565					570					575	
Asp	Gly	Ser	Lys	Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg	Arg
			580					585					590		
Thr	Gly	Tyr	Ser	Trp	Gly	Gly	Ser	Tyr	Gly	Glu	Ser	Ile	Ile	Ser	Phe
		595					600					605			
Ala	Gln	Lys	Val	Gly	Tyr	Leu									
	610					615									

<210> 121
 <211> 1047
 <212> DNA
 <213> Bacteria

<400> 121
 atgatgagat caagcatcgt caagctagtt gctttcagtg ttgtggttat gttatggctc
 60

ggtgtatcct ttcaaacggc agaagcgaat acgccaaatt tcaacttaca aggctttgcc
 120
 acgttaaagt ggggaacaac tgggtggtgca ggtggagatg tagtgacggg tcgtacaggg
 180
 aatgaattaa taaacgcttt gaagtccaaa aaccctaata gtccgttaac aatttatgta
 240
 aacggtacga taacacctag taatacgtct gatagtaaga tcgatattaa ggatgtttcc
 300
 aatgtatcga ttttaggggt tggtaaaaat ggacgattaa atgggatcgg tattaaagta
 360
 tggcgagcga ataatatcat cattcgcaac ttgacgatcc atgaagtcca tacaggatg
 420
 aaagatgcga ttagcattga agggccctct cggaacattt ggattgacca taacgagctt
 480
 tatgccagct tgaacgttca taaagaccac tatgacggct tgtttgacgt aaagcgcgat
 540
 gcttacaata ttaccttctc ttggaattat gtccatgatg gctggaaagc gatgctcatg
 600
 gggaactctg atagtataa ctacgaccga aacataacat tccaccataa ctacttcaa
 660
 aacttaaaact ctgcgtacc tgcgtaccgt tttggaaagg cgcacttgtt tagcaattac
 720
 tttgagaaca ttttagaaac aggcattaat tcacggatgg gagcggaaat gctcgttgaa
 780
 cataacgttt ttgagaatgc caccaaccgg ttaggattct ggcatagcag tcgaacaggt
 840
 tattggaatg ttgccaataa ccgctatatc aatagcacgg gtagcatgcc gaccacttcc
 900
 acgaccaatt atcgacctcc ttatccctat acggtcacac cagttggtga tgtgaaatcg
 960
 gttgtcacac gttatgcggg agttggtgtc atccagccgt atgcaagaaa gccatccgag
 1020
 cgattgctct ggtggctttt tgcataa
 1047

<210> 122
 <211> 348
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(29)

<221> DOMAIN
 <222> (30)...(348)
 <223> Catalytic domain

<400> 122
 Met Met Arg Ser Ser Ile Val Lys Leu Val Ala Phe Ser Val Val Val
 1 5 10 15
 Met Leu Trp Leu Gly Val Ser Phe Gln Thr Ala Glu Ala Asn Thr Pro
 20 25 30
 Asn Phe Asn Leu Gln Gly Phe Ala Thr Leu Asn Gly Gly Thr Thr Gly
 35 40 45
 Gly Ala Gly Gly Asp Val Val Thr Val Arg Thr Gly Asn Glu Leu Ile
 50 55 60
 Asn Ala Leu Lys Ser Lys Asn Pro Asn Arg Pro Leu Thr Ile Tyr Val
 65 70 75 80
 Asn Gly Thr Ile Thr Pro Ser Asn Thr Ser Asp Ser Lys Ile Asp Ile

tctgagaata tcatcatccg aaatatattcg ctgatagggc caggagccgt agatatagac
 600
 ggagctgacc tgattaccaa tcagggtaag cacgtctgga ttgaccattg cacgtttgtg
 660
 gactctcaag atggtgccct ggacagcaag gtatgcgact gggccaccta tacctataac
 720
 cacttctact atacagaccg cagttactca catgcctaca cttgcggttg cggatgggtc
 780
 agcaatcatg aaatgggtgat tcacatgacc tttgcatgta atatctgggg agcaaaatgt
 840
 atgcgtcgtc tgccgcaagc agatgactgt ttcatacacc ttgtgaacaa ctatcacaac
 900
 tgtcctggca atagtgtcgg tatgaccatt aacagttaca gcaaagcatt ggttgagggg
 960
 aactatgctg ctgcaggtgt caacaagcca ttagatggca gtggggccaa ccgtaatgta
 1020
 acagctaagg ataatagttt tgcaaactca caagccgggt ctgttgtgtc tgtgccatac
 1080
 gactatacca agattgcagc cgccgacgtt ccagctacgc tgactggaac agagggtgca
 1140
 ggcgccacat taggcaacga tgcaacatac attctgtcta ctattccaac tgtcgaccga
 1200
 caagaaggcg aatcttctact ctactatttc attgatggcc tgggtgggaac taatagtga
 1260
 ggctattcca ttatagagtt taatgatggc gcaacattgc tgctgaacaa taaagagaaa
 1320
 gcatggtcta atggtagtgc aattcaactt ggtgacgata attatacgag tattaaactt
 1380
 tctaattggag cagaaaaacat cttcacagca cctactggca aaaaagtaag tgggtattacc
 1440
 ttctattctt atatcaatat aaaagaagaa aaactcgact tcaccaaata tccagaatat
 1500
 ggtttccgca cctgtttctg gcagaaaagt gccaacctca cttattctgc gacttctgat
 1560
 gacgtacaaa tcttgaaatc tcgtgatcca cagaatactg acgtggcatc attccatttc
 1620
 actccaacaa atgttgtaag tttcaaaaat tcaggatgaac agctttgttt cttaatgaaa
 1680
 gtcacctata gtgatgaaag cacaggtatc tctgctatcc agaaaaaaat gcctatcgat
 1740
 ggcgttacct ataaccttca aggtatccgt atagataatc ccaccaaggg aatctatatt
 1800
 cagaacggaa agaaaaatcat tatcaaataa
 1830

<210> 124

<211> 609

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(21)

<221> DOMAIN

<222> (22)...(390)

<223> Catalytic domain

<400> 124

Leu	Ser	Leu	Leu	Ser	Val	Met	Thr	Leu	Leu	Pro	Val	Met	Ala	Ser	Asn
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Asn	Val	Ala	Pro	Trp	Gly	Trp	Ala	Thr	Cys	Ser	Asp	Glu	Ser	Ala	Thr
			20					25					30		
Ala	Tyr	Thr	Leu	Asn	Gly	Gly	Cys	Phe	Ser	Asp	Ala	Ser	Ser	Val	Thr
		35					40					45			
Leu	Lys	Ala	Leu	Gly	Asn	Glu	Gln	Thr	Asp	Asp	Lys	Gln	Ile	Lys	Gln
	50					55					60				
Ala	Ile	Ala	Gln	Lys	Asp	Ile	Ile	Ile	Leu	Asp	Gly	Ser	Asn	Gly	Asp
65					70					75				80	
Phe	Ile	Leu	Asn	Glu	Tyr	Ile	Lys	Ile	Ser	Thr	Lys	Asn	Lys	Thr	Ile
				85					90					95	
Ile	Gly	Ile	Asn	Asn	Ala	Arg	Leu	Cys	Thr	Lys	Phe	Tyr	Leu	Thr	Ala
			100					105					110		
Asp	Asp	Ile	Thr	Tyr	Leu	Lys	Ala	Gln	Gly	Leu	Glu	Gly	Leu	Ser	Ser
		115					120					125			
Thr	Asn	Gln	His	Thr	Gly	Thr	Leu	Pro	Asp	Gly	Thr	Thr	Val	Thr	Cys
	130					135						140			
Asp	Glu	Arg	Ala	Phe	Phe	Thr	Lys	Lys	Ala	Ile	Met	Glu	Leu	Gln	Tyr
145					150					155					160
Gln	Lys	Thr	Gly	Ser	Tyr	Thr	Leu	Pro	Asn	Lys	Ser	Gly	Ile	Phe	Tyr
				165					170					175	
Leu	Asp	Ala	Ala	Ser	Glu	Asn	Ile	Ile	Ile	Arg	Asn	Ile	Ser	Leu	Ile
			180					185					190		
Gly	Pro	Gly	Ala	Val	Asp	Ile	Asp	Gly	Ala	Asp	Leu	Ile	Thr	Asn	Gln
		195					200					205			
Gly	Lys	His	Val	Trp	Ile	Asp	His	Cys	Thr	Phe	Val	Asp	Ser	Gln	Asp
	210					215					220				
Gly	Ala	Leu	Asp	Ser	Lys	Val	Cys	Asp	Trp	Ala	Thr	Tyr	Thr	Tyr	Asn
225					230					235					240
His	Phe	Tyr	Tyr	Thr	Asp	Arg	Ser	Tyr	Ser	His	Ala	Tyr	Thr	Cys	Gly
				245					250					255	
Cys	Gly	Trp	Val	Ser	Asn	His	Glu	Met	Val	Ile	His	Met	Thr	Phe	Ala
			260					265					270		
Cys	Asn	Ile	Trp	Gly	Ala	Lys	Cys	Met	Arg	Arg	Leu	Pro	Gln	Ala	Asp
		275					280					285			
Asp	Cys	Phe	Ile	His	Leu	Val	Asn	Asn	Tyr	His	Asn	Cys	Pro	Gly	Asn
	290					295					300				
Ser	Val	Gly	Met	Thr	Ile	Asn	Ser	Tyr	Ser	Lys	Ala	Leu	Val	Glu	Gly
305					310					315					320
Asn	Tyr	Ala	Ala	Ala	Gly	Val	Asn	Lys	Pro	Leu	Asp	Gly	Ser	Gly	Ala
				325					330					335	
Asn	Arg	Asn	Val	Thr	Ala	Lys	Asp	Asn	Ser	Phe	Ala	Asn	Ser	Gln	Ala
			340					345					350		
Gly	Ser	Val	Val	Ser	Val	Pro	Tyr	Asp	Tyr	Thr	Lys	Ile	Ala	Ala	Ala
		355					360					365			
Asp	Val	Pro	Ala	Thr	Leu	Thr	Gly	Thr	Glu	Gly	Ala	Gly	Ala	Thr	Leu
	370					375					380				
Gly	Asn	Asp	Ala	Thr	Tyr	Ile	Leu	Ser	Thr	Ile	Pro	Thr	Val	Asp	Arg
385					390					395					400
Gln	Glu	Gly	Glu	Ser	Ser	Leu	Tyr	Tyr	Phe	Ile	Asp	Gly	Leu	Val	Gly
				405					410					415	
Thr	Asn	Ser	Glu	Gly	Tyr	Ser	Ile	Ile	Glu	Phe	Asn	Asp	Gly	Ala	Thr
			420					425					430		
Leu	Leu	Leu	Asn	Asn	Lys	Glu	Lys	Ala	Trp	Ser	Asn	Gly	Ser	Ala	Ile
		435					440					445			
Gln	Leu	Gly	Asp	Asp	Asn	Tyr	Thr	Ser	Ile	Lys	Leu	Ser	Asn	Gly	Ala
	450					455					460				
Glu	Asn	Ile	Phe	Thr	Ala	Pro	Thr	Gly	Lys	Lys	Val	Ser	Gly	Ile	Thr
465					470					475					480
Phe	Tyr	Ser	Tyr	Ile	Asn	Ile	Lys	Glu	Glu	Lys	Leu	Asp	Phe	Thr	Lys

				485					490					495			
Tyr	Pro	Glu	Tyr	Gly	Phe	Arg	Thr	Cys	Phe	Trp	Gln	Lys	Val	Ala	Asn		
			500					505					510				
Leu	Thr	Tyr	Ser	Ala	Thr	Ser	Asp	Asp	Val	Gln	Ile	Leu	Lys	Ser	Arg		
		515					520					525					
Asp	Pro	Gln	Asn	Thr	Asp	Val	Ala	Ser	Phe	His	Phe	Thr	Pro	Thr	Asn		
	530				535						540						
Val	Val	Ser	Phe	Lys	Asn	Ser	Gly	Glu	Gln	Leu	Cys	Phe	Leu	Met	Lys		
545				550						555					560		
Val	Thr	Tyr	Ser	Asp	Glu	Ser	Thr	Gly	Ile	Ser	Ala	Ile	Gln	Lys	Lys		
			565					570						575			
Met	Pro	Ile	Asp	Gly	Val	Thr	Tyr	Asn	Leu	Gln	Gly	Ile	Arg	Ile	Asp		
		580						585					590				
Asn	Pro	Thr	Lys	Gly	Ile	Tyr	Ile	Gln	Asn	Gly	Lys	Lys	Ile	Ile	Ile		
		595					600						605				
Lys																	

<210> 125
 <211> 1170
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 125
 atgagggtcta aaatcatcag cgccataaat aattatagtg ttattattct cgatggctcg
 60
 aatggcgatt tcactattag tgctacaatg agtttcagta gcaaatcaaa caaaaccata
 120
 gttggtgtaa ataatgctcg cctatgcacc aagttctatc taaccgatga aataaagact
 180
 gcgctcgatg ctgctaattgt aaaatcagca agttcaacca gtggaggtgg tacactctca
 240
 aatgggaaat cagtgtcaga acaacgtgaa taccttactc gtcaaacaat tatcgatcta
 300
 actggcgatg cttcggaatc gtgtcagaaa gcgggcatct ttagcttcag tagttgtacc
 360
 aatatcatca tgcgaaacct cgttttgggt ggccctggcc catgcatgt aggtggcaac
 420
 gatttgcttt cgctcactgg ttctaagcat ttttgggtcg atcactgtga gttaaccgat
 480
 ggtatagatg gcaatttcga tattaccaag agtagcgatt tcaatactgt tacttggtgt
 540
 atattcaatt ataccgatcg tgcatacgac cacatgaact ccaatcttat tggtagctcc
 600
 gatagcgaag atgctgccta tttgaacact actatggcat gcaatatttg gggctacaag
 660
 tgcaatcagc gaatgccaat ggctcgtgct ggtaatatc accttgtgaa caacttttac
 720
 gattgcgctg gcaatagtgt ggctgttaac cctcgtaaaa attctgagtt cttagtcgag
 780
 aactgctact ttgccacggg tgtgaagcca ttctcgaga gtggtgcgtt gggatacaac
 840
 ttattgatt gctatacaga agattcatac acttttcagc agagtgttac agtgtctgtg
 900
 ccatacgttt actctaagtt tgatgtgcaa ttagtaccgg agcaactcaa taaatatgtc
 960
 ggcgcaacgc ttacttctcc gcttgtcata ggtcgggaag aggtgtgtgt tactcctatt
 1020

agtgctgtct ctgttgatag cgatgttggtg ttggtcgaat actattcgct gactggtaat
 1080
 cgtgttaaca cgctcaatag aggcataaat atcgtttagaa ctatttacgc caacggcaaa
 1140
 gtaaccacac aaaaggtttt ggtgaaatag
 1170

<210> 126
 <211> 389
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> DOMAIN
 <222> (24)...(325)
 <223> Catalytic domain

<400> 126
 Met Arg Ser Lys Ile Ile Ser Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1 5 10 15
 Leu Asp Gly Ser Asn Gly Asp Phe Thr Ile Ser Ala Thr Met Ser Phe
 20 25 30
 Ser Ser Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
 35 40 45
 Cys Thr Lys Phe Tyr Leu Thr Asp Glu Ile Lys Thr Ala Leu Asp Ala
 50 55 60
 Ala Asn Val Lys Ser Ala Ser Ser Thr Ser Gly Gly Gly Thr Leu Ser
 65 70 75 80
 Asn Gly Lys Ser Val Ser Glu Gln Arg Glu Tyr Leu Thr Arg Gln Thr
 85 90 95
 Ile Ile Asp Leu Thr Gly Asp Ala Ser Glu Ser Cys Gln Lys Ala Gly
 100 105 110
 Ile Phe Ser Phe Ser Ser Cys Thr Asn Ile Ile Met Arg Asn Leu Val
 115 120 125
 Leu Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu Ser
 130 135 140
 Leu Thr Gly Ser Lys His Phe Trp Val Asp His Cys Glu Leu Thr Asp
 145 150 155 160
 Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn Thr
 165 170 175
 Val Thr Trp Cys Ile Phe Asn Tyr Thr Asp Arg Ala Tyr Asp His Met
 180 185 190
 Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asp Ala Ala Tyr Leu
 195 200 205
 Asn Thr Thr Met Ala Cys Asn Ile Trp Gly Tyr Lys Cys Asn Gln Arg
 210 215 220
 Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Phe Tyr
 225 230 235 240
 Asp Cys Ala Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser Glu
 245 250 255
 Phe Leu Val Glu Asn Cys Tyr Phe Ala Thr Gly Val Lys Pro Phe Ser
 260 265 270
 Gln Ser Gly Ala Leu Gly Tyr Asn Phe Ile Asp Cys Tyr Thr Glu Asp
 275 280 285
 Ser Tyr Thr Phe Gln Gln Ser Gly Thr Val Ser Val Pro Tyr Val Tyr
 290 295 300
 Ser Lys Phe Asp Val Gln Leu Val Pro Glu Gln Leu Asn Lys Tyr Ala
 305 310 315 320
 Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Glu Gly Val

325 330 335
 Val Thr Pro Ile Ser Ala Val Ser Val Asp Ser Asp Val Val Leu Val
 340 345 350
 Glu Tyr Tyr Ser Leu Thr Gly Asn Arg Val Asn Thr Leu Asn Arg Gly
 355 360 365
 Ile Asn Ile Val Arg Thr Ile Tyr Ala Asn Gly Lys Val Thr Thr Gln
 370 375 380
 Lys Val Leu Val Lys
 385

<210> 127
 <211> 1449
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 127
 atgcaatatg gcaaattagt acgcttgtcg gcactgacaa cagcgctggc attcagcgcc
 60
 ctggcacagg caaataacct ggcaattaca ggccccggag ccggggctga tggttccagc
 120
 aaagccagtg gcagtagcta cggcgatgta aaagacgccg atctgcaaag ctactggcaa
 180
 ccgcctgcta ataacggcca aagagtgtcg gttaagtgga gcagcgctat cagcgttaat
 240
 caggtaatac tgcgtgaaca gggcagtaat gtaaccagct ggcggtggt aaataatgac
 300
 aacggcgagcag tattggcaac cggcaccagc attggcagca acagaacggt taacttcagc
 360
 actgtaagca cgaaaaaact caatctggaa atactaactg ccagcggtgc cccgcgcatt
 420
 gctgagtttg aagtttattt aaataccaat ggcggaacc cgccaaatcc tactgacccg
 480
 gaaccaggcc cggtaaactt ttgcgcagcg tctccacagg gctatgcctc gcttaacggt
 540
 ggcaactaccg gcggcagtgg cagcaacgcg gtcacggtaa cggtaagcac cggcgctcaa
 600
 atggtatcgg cgctacaaaa ccgcgatcta aaccggccgc tcactatccg ggttaatggc
 660
 actatcacac cgggtaattc tggcggtgtc agtaagtttg acattaaaga tatggataat
 720
 gtcagcatta ttggtgtagg caacaatgcg ttgtttgacg gtatcggtat taaaatctgg
 780
 cgggccaata acgttattat ccgcaacctt acaatgcgtt atgttaacac cggcgataaa
 840
 gacgtatta ccattgaagg cccggcgcggt aatatctgga ttgaccacaa cgaaatctat
 900
 aacagcctga atgtgggtaa agatttttac gacgagctta taagcggtaa aaaagacgta
 960
 gataacgtaa ctatctctta caactacctg cacgacagct ggaaaacctc gctgtggggc
 1020
 agcagtgatt ccgacaacta caaccgccgt attacctttc accataacca ctggcataag
 1080
 gtaaattcac gcctgccact gttccgtttt ggccagggcc atatttacia taactattac
 1140
 aacgacattc aggacaccgg tattaacagc cggatgggtg cggtaattcg tattgaaaac
 1200
 aatgtgtttg aaaacgcgaa aaacccgata gtgtcgtttt attccagcgg ctacggttac
 1260

tgggacaccc gcggtaatag ctttagcaat attacctggc aggaataccc cagcgacggc
 1320
 attatcgccg ggccaaatgt acaaccacaca gcggtgctaa acctgcccta cagctttaac
 1380
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 1440
 agtttctaa
 1449

<210> 128
 <211> 482
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(24)
 <221> DOMAIN
 <222> (5)...(482)
 <223> Catalytic domain

<400> 128
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 Ala Phe Ser Ala Leu Ala Gln Ala Asn Asn Leu Ala Ile Thr Gly Pro
 20 25 30
 Gly Ala Gly Ala Asp Gly Ser Ser Lys Ala Ser Gly Ser Ser Tyr Gly
 35 40 45
 Asp Val Lys Asp Ala Asp Leu Gln Ser Tyr Trp Gln Pro Pro Ala Asn
 50 55 60
 Asn Gly Gln Arg Val Ser Val Lys Trp Ser Ser Ala Ile Ser Val Asn
 65 70 75 80
 Gln Val Ile Leu Arg Glu Gln Gly Ser Asn Val Thr Ser Trp Arg Leu
 85 90 95
 Val Asn Asn Asp Asn Gly Ala Val Leu Ala Thr Gly Thr Ser Ile Gly
 100 105 110
 Ser Asn Arg Thr Val Asn Phe Ser Thr Val Ser Thr Lys Lys Leu Asn
 115 120 125
 Leu Glu Ile Leu Thr Ala Ser Gly Ala Pro Arg Ile Ala Glu Phe Glu
 130 135 140
 Val Tyr Leu Asn Thr Asn Gly Gly Asn Pro Pro Asn Pro Thr Asp Pro
 145 150 155 160
 Glu Pro Gly Pro Val Thr Ser Cys Ala Ala Ser Pro Gln Gly Tyr Ala
 165 170 175
 Ser Leu Asn Gly Gly Thr Thr Gly Gly Ser Gly Ser Asn Ala Val Thr
 180 185 190
 Val Thr Val Ser Thr Gly Ala Gln Met Val Ser Ala Leu Gln Asn Arg
 195 200 205
 Asp Leu Asn Arg Pro Leu Thr Ile Arg Val Asn Gly Thr Ile Thr Pro
 210 215 220
 Gly Asn Ser Gly Gly Val Ser Lys Phe Asp Ile Lys Asp Met Asp Asn
 225 230 235 240
 Val Ser Ile Ile Gly Val Gly Asn Asn Ala Leu Phe Asp Gly Ile Gly
 245 250 255
 Ile Lys Ile Trp Arg Ala Asn Asn Val Ile Ile Arg Asn Leu Thr Met
 260 265 270
 Arg Tyr Val Asn Thr Gly Asp Lys Asp Ala Ile Thr Ile Glu Gly Pro
 275 280 285

Ala	Arg	Asn	Ile	Trp	Ile	Asp	His	Asn	Glu	Ile	Tyr	Asn	Ser	Leu	Asn
290						295					300				
Val	Gly	Lys	Asp	Phe	Tyr	Asp	Glu	Leu	Ile	Ser	Gly	Lys	Lys	Asp	Val
305					310					315					320
Asp	Asn	Val	Thr	Ile	Ser	Tyr	Asn	Tyr	Leu	His	Asp	Ser	Trp	Lys	Thr
				325					330					335	
Ser	Leu	Trp	Gly	Ser	Ser	Asp	Ser	Asp	Asn	Tyr	Asn	Arg	Arg	Ile	Thr
			340					345					350		
Phe	His	His	Asn	His	Trp	His	Lys	Val	Asn	Ser	Arg	Leu	Pro	Leu	Phe
		355					360					365			
Arg	Phe	Gly	Gln	Gly	His	Ile	Tyr	Asn	Asn	Tyr	Tyr	Asn	Asp	Ile	Gln
	370				375						380				
Asp	Thr	Gly	Ile	Asn	Ser	Arg	Met	Gly	Ala	Val	Ile	Arg	Ile	Glu	Asn
385					390					395					400
Asn	Val	Phe	Glu	Asn	Ala	Lys	Asn	Pro	Ile	Val	Ser	Phe	Tyr	Ser	Ser
				405					410					415	
Gly	Tyr	Gly	Tyr	Trp	Asp	Thr	Arg	Gly	Asn	Ser	Phe	Ser	Asn	Ile	Thr
			420					425					430		
Trp	Gln	Glu	Tyr	Pro	Ser	Asp	Gly	Ile	Ile	Ala	Gly	Pro	Asn	Val	Gln
		435					440					445			
Pro	Thr	Ala	Val	Leu	Asn	Leu	Pro	Tyr	Ser	Phe	Asn	Leu	Leu	Pro	Thr
	450					455					460				
Asn	Gln	Val	Lys	Ala	His	Val	Leu	Ala	Asn	Ala	Gly	Val	Asn	Lys	Cys
465					470					475					480
Ser	Phe														

<210> 129

<211> 1173

<212> DNA

<213> Bacillus halodurans ATCC 27557

<220>

<400> 129

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120
gtgggtgtga acaatgctcg cctatgcacc aaattctaca ttacgcccga gataaaagaa
180
gccctcgatg ctgccgatgt gaaatctaag agctcaagta gtggcactgg tggaaactctt
240
tctaattgga cgtcggtcag tgaggctcgc gaattggcta ctcgtaaac gttgattgat
300
tatctcggcg atagctcaga atcgtatcag aaagctggta tctttggctt tagcaactgc
360
actaatatta ttatgcgcaa cattgttttc gttggccctg gtccatgcga tgtaggtggc
420
aacgacttgc tttcgctcgt tggttcgaag catttctggg tcgaccactg cgagtttacc
480
gatggcatcg atggcaactt cgacatcacc aagagtagcg acttcaacac cgtttcgtgg
540
tgcactttca gctataccga ccgcgcatac gaccacatga attccaacct tattggtagc
600
tccgattcag agaatgcggc ttaccttaat actactatgg cttccaacgt ctggggcaat
660
aagtgaatc agcgtatgcc tatggctcgt gccggaata ttcacctcgt aaataattat
720
tacaactgcc ctggcaatag cgtggctgtg aatcctcgca aaaactcaga atttttggtg
780

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gagaattgct atttcgcaag tggcggttaag cttttctcgc agagcggcgc tcttagctat
 840
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 900
 gtgccatata catatagcaa attcgatgct cagcttggtc ccgagcaact caccgaattc
 960
 gctggcgcaa cattgacttc gccgcttggt attggtaggg aatctgagaa tggttacacca
 1020
 gtctcagtc tttgtgcaaa tagcgatgtc atatctgtag aatactattc gctcactggc
 1080
 aagcgcacga gcgaaccaac taaaggcatc aatatcggtt gaactattta tactaacggc
 1140
 aacgtgacca cacaaaaggc cttggtgaaa taa
 1173

<210> 130
 <211> 390
 <212> PRT
 <213> Bacillus halodurans ATCC 27557

<220>

<221> DOMAIN
 <222> (38)...(326)
 <223> Catalytic domain

<400> 130
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 Leu Asp Gly Ser Asn Gly Asp Phe Thr Val Asn Ala Thr Met Ser Phe
 20 25 30
 Ser Gly Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
 35 40 45
 Cys Thr Lys Phe Tyr Ile Thr Pro Glu Ile Lys Glu Ala Leu Asp Ala
 50 55 60
 Ala Asp Val Lys Ser Lys Ser Ser Ser Ser Gly Thr Gly Gly Thr Leu
 65 70 75 80
 Ser Asn Gly Thr Ser Val Ser Glu Ala Arg Glu Leu Ala Thr Arg Gln
 85 90 95
 Thr Leu Ile Asp Tyr Leu Gly Asp Ser Ser Glu Ser Tyr Gln Lys Ala
 100 105 110
 Gly Ile Phe Gly Phe Ser Asn Cys Thr Asn Ile Ile Met Arg Asn Ile
 115 120 125
 Val Phe Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu
 130 135 140
 Ser Leu Val Gly Ser Lys His Phe Trp Val Asp His Cys Glu Phe Thr
 145 150 155 160
 Asp Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn
 165 170 175
 Thr Val Ser Trp Cys Thr Phe Ser Tyr Thr Asp Arg Ala Tyr Asp His
 180 185 190
 Met Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asn Ala Ala Tyr
 195 200 205
 Leu Asn Thr Thr Met Ala Ser Asn Val Trp Gly Asn Lys Cys Asn Gln
 210 215 220
 Arg Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Tyr
 225 230 235 240
 Tyr Asn Cys Pro Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser
 245 250 255
 Glu Phe Leu Val Glu Asn Cys Tyr Phe Ala Ser Gly Val Lys Pro Phe
 260 265 270

Ser Gln Ser Gly Ala Leu Ser Tyr Leu Phe Ile Asp Cys Tyr Thr Glu
 275 280 285
 Asp Thr Tyr Thr Phe Gln Lys Ser Gly Ser Thr Thr Val Pro Tyr Thr
 290 295 300
 Tyr Ser Lys Phe Asp Ala Gln Leu Val Pro Glu Gln Leu Thr Gln Phe
 305 310 315 320
 Ala Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Ser Glu
 325 330 335
 Asn Val Thr Pro Val Ser Val Ile Ala Ala Asn Ser Asp Val Ile Ser
 340 345 350
 Val Glu Tyr Tyr Ser Leu Thr Gly Lys Arg Ile Ser Glu Pro Thr Lys
 355 360 365
 Gly Ile Asn Ile Val Arg Thr Ile Tyr Thr Asn Gly Asn Val Thr Thr
 370 375 380
 Gln Lys Val Leu Val Lys
 385 390

<210> 131
 <211> 972
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 131
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 120
 tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag cgacagcggc
 180
 accatcgaca atggtgcaac cattaccgaa atgggtttacc tcgctgaaat ttataaaaaac
 240
 ggcggcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg
 300
 caatacagca caggcgcctt gccacaattt tatccgttga aaggcgggcta tgcggatcat
 360
 gcgaccttta acgataacgg catggcgtag gcgttgacgg tattggattt cgcagtaaac
 420
 aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaaacc
 480
 gctgttgcca aaggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaactc
 540
 actgcatggt gtgcacaaca cgggtgctacg gattaccaac cgaaaaaagc gcgcgcttat
 600
 gaattggaat cattgagtgg tagcgagtcg gtcggcattc tcgccttctt gatgacccaa
 660
 ccacaaaccg cgcaaatacga agcggcggtc aaggcgggtg tcaactgggt cgccagtcca
 720
 aatacttatt tggctaacta cacttacgat tcatcaaaaag cgtctaccaa cccgattgtg
 780
 tataaatccg gaagcagaat gtggtatcgc ttctatgacc tgaacaccaa ccgtggtttc
 840
 tttagtgatc gcgatggcag caaattctat gatatcacc aaatgtcaga agagcgtcgc
 900
 accggttata gctgggggtg ctcttacggt gaatctatta tttccttcgc gcaaaaagt
 960
 ggttatctgt ag
 972

<210> 132
<211> 323
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 132
Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
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Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
20 25 30
Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
35 40 45
Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
50 55 60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
65 70 75 80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
85 90 95
Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
100 105 110
Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met
115 120 125
Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro
130 135 140
Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala Lys Phe Lys Thr
145 150 155 160
Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln
165 170 175
Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Thr Asp Tyr
180 185 190
Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser
195 200 205
Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
210 215 220
Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
225 230 235 240
Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
245 250 255
Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp Tyr Arg Phe Tyr
260 265 270
Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys
275 280 285
Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser
290 295 300
Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe Ala Gln Lys Val
305 310 315 320
Gly Tyr Leu

<210> 133
<211> 972
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated polynucleotide

<400> 133

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 120
 tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag cgacagcggc
 180
 accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat ttataaaaac
 240
 ggccgcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg
 300
 caatacagca caggcgcctt gccacaattt tatccgttga aaggcggcta tcatgatcat
 360
 gcgaccttta acgataacgg catggcgtag gcgttgacgg tattggattt cgacagtaaac
 420
 aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaacc
 480
 gctgttgcca aagggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaaactc
 540
 actgcatggt gtgcacaaca cggtgctttg gattaccaac cgaaaaaagg tcgcgcttat
 600
 gaattggaat cattgagtgg taaggagtcg gtcggcattc tcgccttctt gatgacccaa
 660
 ccacaaaccg cgcaaatcga agcggcggtc aaggcgggtg tcaactgggt cgccagtcca
 720
 aatacttatt tggctaacta cacttacgat tcatcaaaaag cgtctaccaa cccgattgtg
 780
 tataaaaagg gaagcagaat gtggtatcgc ttctatgacc tgtataccea ccgtgggttc
 840
 tttagtgatc gcgatggcag caaattctat gatatcacc aaatgtcaga agagcgtcgc
 900
 accggttata gctgggggtg ctcttggggt gaagttatta tttccttcgc gcaaaaagt
 960
 ggttatctgt ag
 972

<210> 134

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated polypeptide

<400> 134

Met	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro	Ala	Ala	Ser	Trp	Phe
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			20					25					30		
Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys	Asn	Leu	Asp	Tyr	Asn
		35				40						45			
Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser	Gly	Thr	Ile	Asp	Asn
	50					55					60				
Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala	Glu	Ile	Tyr	Lys	Asn
65					70				75					80	
Gly	Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg	Arg	Ala	Ala	Asn	Phe
			85						90					95	
Leu	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu	Pro	Gln	Phe	Tyr	Pro
			100					105				110			
Leu	Lys	Gly	Gly	Tyr	His	Asp	His	Ala	Thr	Phe	Asn	Asp	Asn	Gly	Met
		115				120					125				
Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val	Asn	Lys	Arg	Ala	Pro

130		135		140
Phe Asp Asn Asp Ile	Phe Ser Asp Ser Asp Arg	Ala Lys Phe Lys Thr		
145	150	155	160	
Ala Val Ala Lys Gly	Val Asp Tyr Ile Leu	Lys Ala Gln Trp Lys Gln		
	165	170	175	
Asn Gly Lys Leu Thr	Ala Trp Cys Ala Gln	His Gly Ala Leu Asp Tyr		
	180	185	190	
Gln Pro Lys Lys Gly	Arg Ala Tyr Glu Leu	Glu Ser Leu Ser Gly Lys		
	195	200	205	
Glu Ser Val Gly Ile	Leu Ala Phe Leu Met	Thr Gln Pro Gln Thr Ala		
	210	215	220	
Gln Ile Glu Ala Ala	Val Lys Ala Gly Val	Asn Trp Phe Ala Ser Pro		
225	230	235	240	
Asn Thr Tyr Leu Ala	Asn Tyr Thr Tyr Asp	Ser Ser Lys Ala Ser Thr		
	245	250	255	
Asn Pro Ile Val Tyr	Lys Lys Gly Ser Arg	Met Trp Tyr Arg Phe Tyr		
	260	265	270	
Asp Leu Tyr Thr Asn	Arg Gly Phe Phe Ser	Asp Arg Asp Gly Ser Lys		
	275	280	285	
Phe Tyr Asp Ile Thr	Gln Met Ser Glu Glu	Arg Arg Thr Gly Tyr Ser		
	290	295	300	
Trp Gly Gly Ser Trp	Gly Glu Val Ile Ile	Ser Phe Ala Gln Lys Val		
305	310	315	320	
Gly Tyr Leu				